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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 17:16:18 : Search time 937.26 seconds
(without alignments)
2194.834 Million cell updates/sec

Title: US-09-050-249-1
Perfect score: 471
Sequence: 1 AACCTTGCCGACCTTCACTG.....TCACCTACTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1034670 seqs, 2183789903 residues
Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
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8: gb_pl2: *
9: gb_pl1: *
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17: em_hum2: *
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26: em_sts: *
27: em_sy: *
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33: gb_in3: *
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91: gb_sts1: *
92: gb_sts2: *
93: gb_vl1: *
94: gb_vl2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	99.9	471	5	AR072044
2	470.6	99.9	471	5	E13264 Mouse cDNA
3	470.6	99.9	471	5	E14257 CDNA encodi
4	470.6	99.9	471	5	E14760 CDNA encodi
5	470.6	99.9	471	5	E17139 Murine mRNA
6	470.6	99.9	471	22	E10609 Mouse cDNA
7	470.6	99.9	471	22	E11744 CDNA encodi
8	470.6	99.9	471	22	E12010 CDNA encodi
9	470.6	99.9	866	12	MUSGIFPP DA9949 Mouse mRNA
10	452	96.0	572	12	MMU66244 Mus musculu
11	400.6	85.1	722	12	RNU77776 Rattus norv
12	395.8	84.0	628	12	RAJ22813 Rattus no

13	392.4	83.3	483	12	RN13337	Y13337 Rattus norv
14	279.8	59.4	665	12	RN07777	U77777 Rattus norv
15	279.8	59.3	471	13	ASIGIF	Y09278 Artificial
16	268.4	57.0	582	3	ECIGIF	Y11311 Equus caball
17	254	53.9	534	3	AF173175	AF173175 Bos tauru
18	254	53.9	754	3	AF124789	AF124789 Bos tauru
19	247.8	52.6	471	5	E17135	E17135 Human mRNA
20	247.8	52.6	579	66	HS090434	U90434 Human inter
21	247.8	52.6	1102	35	D49950	D49950 Homo sapien
22	247.4	52.5	471	5	E13265	E13265 Human cDNA
23	247.4	52.5	471	5	E15793	E15793 Human cDNA
24	247.4	52.5	471	22	E12009	E12009 cDNA encodi
25	247.4	52.5	579	3	AR069452	AR069452 Sequence
26	247.4	52.5	579	5	E15603	E15603 cDNA encodi
27	247.4	52.5	1120	5	E14759	E14759 cDNA encodi
28	247.4	52.5	1120	5	E15641	E15641 Human mRNA
29	247.4	52.5	1120	22	E11745	E11745 cDNA encodi
30	247	52.4	589	11	AF077611	AF077611 Homo sapi
31	244.6	51.9	471	5	E17136	E17136 IGIF/MUT35
32	244.4	51.9	579	3	AF191088	AF191088 Sus scrofa
33	244.4	51.9	579	3	SSIGIF	Y11132 Sus scrofa
34	244.4	51.9	582	3	CFIGIF	Y11133 Canis famli
35	244.4	51.9	600	3	SS068701	U68701 Sus scrofa
36	244.4	51.9	665	3	AB010003	AB010003 Sus scrofa
37	243	51.6	471	5	E17137	E17137 IGIF/MUT42
38	242.2	51.4	600	3	AF176949	AF176949 Sus scrofa
39	225	47.8	110931	79	AC027079	AC027079 Mus muscu
40	225	47.8	112150	78	AC025500	AC025500 Mus muscu
41	127.8	27.1	11464	5	E15652	E15652 Human gene
42	127.8	27.1	11464	5	E17138	E17138 Human gene
43	127.8	27.1	28994	5	E15653	E15653 Human gene
44	127.8	27.1	161920	89	AP002502	AP002502 Homo sapi
45	127.8	27.1	165548	89	AP002007	AP002007 Homo sapi

ALIGNMENTS

RESULT	1					
LOCUS	AR072044	471 bp	DNA	PAT	18-FEB-2000	
DEFINITION	Sequence 1 from patent US 5912324.					
ACCESSION	AR072044					
VERSION	AR072044.1	GI:7222932				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 471)					
AUTHORS	Okamura, H., Tanimoto, T., Torigoe, K., Kunikata, T., Taniguchi, M., Kohno, K. and Kurimoto, M.					
TITLE	Interferon-gamma (IFN-gamma.) inducing factor (IGIF, IL-18)					
JOURNAL	Purified from murine liver					
FEATURES	Location/Qualifiers					
Source	1..471					
BASE COUNT	162 a	91 c	92 g	125 t	1 others	
ORIGIN						

Query Match 99.9%; Score 470.6; DB 5; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AACTTTGGCCACTTCATGTACCAACCCAGTATACGGAATATTAATGACCAAGTCTC	60
DB	1	AACTTTGGCCACTTCATGTACCAACCCAGTATACGGAATATTAATGACCAAGTCTC	60
QY	61	TTGCTTGACAAAGACACCGCTGTGTCGAGATATGACTGATATGATCAAGTCCAGT	120
DB	61	TTGCTTGACAAAGACACCGCTGTGTCGAGATATGACTGATATGATCAAGTCCAGT	120

QY	121	GAACCCAGACACGCTGATATATACATGTACAAAGACAGTGAAGTACGAGCTGCT	180
DB	121	GAACCCAGACACGCTGATATATACATGTACAAAGACAGTGAAGTACGAGCTGCT	180
QY	181	GTGACCCCTCTCTGTGAAGAGTATTAAGTCTACCCCTCTCTGTGAAGACAGTATT	240
DB	181	GTGACCCCTCTCTGTGAAGAGTATTAAGTCTACCCCTCTCTGTGAAGACAGTATT	240
QY	241	TCCTTTGAGAAATGATGATCCACCTGAAATATTTGATGATATACAAAGTATTCAT	300
DB	241	TCCTTTGAGAAATGATGATCCACCTGAAATATTTGATGATATACAAAGTATTCAT	300
QY	301	TTTCAGAAACGCTTTCAGACACACACAGATGAGTTGATGATTTTCAAGTATGAAGA	360
DB	301	TTTCAGAAACGCTTTCAGACACACACAGATGAGTTGATGATTTTCAAGTATGAAGA	360
QY	361	CACCTTTCTGCTTCCCAAAAGAGATGATGCTTCAACTATTTGAAAAAAGAT	420
DB	361	CACCTTTCTGCTTCCCAAAAGAGATGATGCTTCAACTATTTGAAAAAAGAT	420
QY	421	GAAATGGGATTAATCTGTAATGTTCTACTCTCACTACTTACATCAAAAGT	471
DB	421	GAAATGGGATTAATCTGTAATGTTCTACTCTCACTACTTACATCAAAAGT	471

RESULT	2					
LOCUS	E13264	471 bp	DNA	PAT	24-JUN-1998	
DEFINITION	Mouse cDNA encoding a protein that induces to produce					
ACCESSION	E13264					
VERSION	E13264.1	GI:3252069				
KEYWORDS	JP 1997157180-A/2.					
SOURCE	Mus sp.					
ORGANISM	Mus sp.					

REFERENCE	1 (bases 1 to 471)					
AUTHORS	Torigoe, K., Tanimoto, T., Fukuda, S. and Kurimoto, M.					
TITLE	AGENT FOR SENSITIVE DISEASE					
JOURNAL	PATENT: JP 1997157180-A 2 17-JUN-1997;					
COMMENT	HAYASHIBARA BIOCHEM LAB INC					
OS	Mus sp. (mouse)					
PN	JP 1997157180-A/2					
PR	17-JUN-1997					
PR	24-JAN-1996 JP 1996028722					
PR	10-MAR-1995 JP 95P 279906					
PI	04-OCT-1995 JP 95P 78357, 29-SEP-1995 JP 95P 274988, PR					
PI	TORIGOE KAKUJI, TANIMOTO TADAO, FUKUDA SHIGETSU, PI					
PI	KURIMOTO MASASHI					
PC	A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00,C07K14/52;					
PC	C07K14/54;					
PC	C07K14/55;					
CC	strandedness: Double;					
CC	topology: Linear;					
CC	Feature is identified by similarity;					
FH	Key					
FH	Location/Qualifiers					
FT	source					
FT	1..471					
FT	/organism="Mus sp."					
FT	/tissue_type="liver"					
FT	mat-peptide					
FT	1..471					
FT	/product="interferon-gamma inducer protein"					
FT	Location/Qualifiers					
FT	1..471					
FT	/db_xref="taxon:10095"					

BASE COUNT	162 a	91 c	92 g	125 t	1 others	
ORIGIN						

Query Match 99.9%; Score 470.6; DB 5; Length 471;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;

FEATURES		factor'
SOURCE	Location/Qualifiers	
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	/db_xref="taxon:10095"	
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ORIGIN		
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Best Local Similarity	100.0%; Pred. No. 1.3e-103;	
Matches 471:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 AACTTGGCCGACCTTCACTGTACAAACCAGTAATAGCATATAAAGACCAAGTTCTC 60	
DB	1 AACTTGGCCGCCTTCCTGATGCAACCCAGTAATAGCGAATATAAAGACCAAGTTCTC 60	
OY	61 TTGCGTGCAAAAAGACAGCGCTGTGTCGAGGATATGATGATATGATCAAGTCCCAGT 120	
DB	61 TTGCGTGCAAAAAGACAGCGCTGTGTCGAGGATATGATGATATGATCAAGTCCCAGT 120	
OY	121 GAACCCGACAGACAGCTGAT 180	
DB	121 GAACCCGACAGACAGCTGAT 180	
OY	181 GTGACCCCTCTCTGTGAAGATATGTAAGAAYGTCTAACCTCTCTGTGAAGAACAAGTCAAT 240	
DB	181 GTGACCCCTCTCTGTGAAGATATGTAAGAAYGTCTAACCTCTCTGTGAAGAACAAGTCAAT 240	
OY	241 TCCCTTGAGGAATGGATGCCACCTGAAAAATATGATATATATCAAAAGATGTCATATTC 300	
DB	241 TCCCTTGAGGAATGGATGCCACCTGAAAAATATGATATATATCAAAAGATGTCATATTC 300	
OY	301 TTTCGAAACAGGTGTCCAGACACACAAGATGAGATTGTAATCTTCACTGATGAGA 360	
DB	301 TTTCGAAACAGGTGTCCAGACACACAAGATGAGATTGTAATCTTCACTGATGAGA 360	
OY	361 CACTTCTTCTGCTTCCCAAAGAGAGATGCTTTCAAACTCATTTCTGAAAAAAAAGAT 420	
DB	361 CACTTCTTCTGCTTCCCAAAGAGAGATGCTTTCAAACTCATTTCTGAAAAAAAAGAT 420	
OY	421 GAAATGGGGAATAATCTGTATGTCTCACTCTCACTAATCTCATCAATCAAGT 471	
DB	421 GAAATGGGGAATAATCTGTATGTCTCACTCTCACTAATCTCATCAATCAAGT 471	
RESULT 4		
E14760	471 bp DNA PAT 28-JUL-1999	
LOCUS	CDNA encoding polypeptide which induces interferon-gamma production	
DEFINITION	HIGIF.	
ACCESSION	E14760 GI:5709443	
VERSION	JP 1998007699-A 13-JAN-1998;	
KEYWORDS	Mus sp.	
SOURCE	Mus sp.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	Ushio,S., Torigoe,K., Tanimoto,T., Okamura,H. and Kurimoto,M. POLYPEPTIDE INDUCING PRODUCTION OF INTERFERON-GAMMA Patent: JP 1998007699-A 13-JAN-1998;	
AUTHORS	HAYASHIBARA BIOCHEM LAB INC	
TITLE	OS Mus sp. (mouse)	
JOURNAL	PJ JP 1998007699-A/2	
COMMENT	PD 13-JAN-1998	
	PF 18-SEP-1995 JP 1997058547	
	PR 15-NOV-1994 JP 94P 304203	
	PI USHIO SHINEI, TORIGOE KAKUI, TANIMOTO TADAO, OKAMURA HARUKI, KI KURIMOTO MASASHI	
	PC COTK14/52,COTR21/04,C12N1/21,C12N15/09,C12P21/02//A6IK8/00, C12R1/21,	
	(C12P21/02,C12R1:19);	

DE Mouse cDNA encoding a protein involved in interferon-gamma production
XX
KM
XX JP 1996027189-A/1.
XX

Db	421	GAAATGGGGAATCTGTATCTTACTCTCTACTTACTTCAAGT	471
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XX ID	E11744	, standard; RNA; ROD; 471 BP.	
AC E11744;			
XX SV	E11744.1		
DT 08-OCT-1997 (Rel. 52, Created)			
DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)			
XX cDNA encoding polypeptide which induce mouse interferon-gamma product.			
DE JP 1996193098-A/1.			
XX Mus musculus (house mouse)			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia			
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
XX [1]			
RP 1-471			
RA Ushio S., Torigoe K., Tanimoto T., Okamura H., Kurimoto M.;			
RT "POLYPEPTIDE FOR INDUCING PRODUCTION OF INTERFERON-GAMMA";			
RL Patent number JP 1996193098-A/1, 30-JUL-1996.			
RN HAYASHIBARA BIOCHEM LAB INC.			
XX OS Mus musculus (mouse)			
CC PN JP 1996193098-A/1			
CC PD 30-JUL-1996			
CC PF 18-SEP-1995 JP 1995262062			
CC PI 15-NOV-1994 JP 94P 304203			
CC PI USHIO SHINPEI, TORIGOE KAKUJI, TANIMOTO TADAO, OKAMURA HARUKI,			
CC PI KURIMOTO MASASHI			
CC PC C07K14/52, C07H21/04, C12N1/21, C12N15/09, C12P21/00//A61K38/00,			
CC PC C07K1/06,			
CC PC C07K1/08, (C12N1/21, C12R1:19), (C12P21/00, C12R1:19);			
CC CC strandedness: Double;			
CC CC topology: Linear;			
CC CC hypothetical: No;			
CC CC anti-sense: No;			
CC FH key Location/Qualifiers			
CC EH source 1..471			
CC FT /db_xref="taxon:10090"			
CC FT /organism="Mus musculus"			
CC FT tissue_type="liver"			
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FT /organism="Mus musculus"			
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Query Match 99.9%; Score 470.6; DB 22; Length 471;			
Best Local Similarity 100.0%; Pred. No. 1.3e-103;			
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY 1 AACTTGGCCACTTCCTACTGTACAACCGCATTAATACGAATAATTAAGCAAGTTCTC 60			
DB 1 AACTTGGCCACTTCCTACTGTACAACCGCATTAATACGAATAATTAATGACCAGTTCTC 60			
OY 61 TTCGTTGCAAAAAGACACCGCTGTGTGGAGATATGACTGATATTGATCAAAAGTGCCAGT 120			
DB 61 TTCGTTGCAAAAAGACACCGCTGTGTGGAGATATGACTGATATTGATCAAAAGTGCCAGT 120			
OY 121 GAACCCGACACAGCATATATATACATGTACAAAGAAGTAGAAGGAGACGCGCT 180			

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FT			/organism="Mus musculus"
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	Query Match	99.9%; Score 470.6; DB 22; Length 471;	
	Best Local Similarity	100.0%; Pred. No. 1.3e-103;	
	Matches 471; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1	AACTTGGCCGACTTCTACTGTACACACCCGAGTAATAGCAATATATAATGACCAAGTCTC	60
Db	1	AACTTGGCCGACTTCTACTGTACACACCCGAGTAATAGCAATATATAATGACCAAGTCTC	60
QY	61	TTTCGTGACAAAGACAGCCTGTGTCGAGATATAGCTGATATTGATCAAAAGTCCAGT	120
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QY	121	GAACCCGACGACGAGTGTATATATACATGTACAAAGACAGTGAAGTAAGAGAGCTGGCT	180
Db	121	GAACCCGACGACGAGTGTATATATACATGTACAAAGACAGTGAAGTAAGAGAGCTGGCT	180
QY	181	GTGACCCCTCTCTGTGAAGATAGTAAAAVGTCTACCCCTCTCTCTTAAGAACAGATCAT	240
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QY	361	CACCTTCTGTCTGTGCGCAAAAGCAAAATATGCTTTCAACATCATTCGAAAAAAAAGAT	420
Db	361	CACCTTCTGTCTGTGCGCAAAAGCAAAATATGCTTTCAACATCATTCGAAAAAAAAGAT	420
QY	421	GAAATGGGATTAATCTGATATGTTCACTCTCACTACTACTACTCAACTCAAGT	471
Db	421	GAAATGGGATTAATCTGATATGTTCACTCTCACTACTACTACTACTCAACTCAAGT	471
RESULT	9		
MUSGIEFP	866 bp	MRNA	10-FEB-1999
LOCUS			
DEFINITION	Mouse mRNA for IGF1 precursor polypeptide, complete cds.		
ACCESSION	D49949		
VERSION	D49949.1 GI:1064822		
KEYWORDS	IGF1 precursor polypeptide.		
SOURCE	Mus musculus liver cDNA to mRNA, clone pMUGF37B-5.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 866)		
TITLE	Okamura, H.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (29-MAR-1995) to the DDBJ/EMBL/GenBank databases. Haruki Okamura, Hyogo College of Medicine, Department of Bacteriology; Mukogawa 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6111)		
AUTHORS	2 (bases 1 to 866)		
TITLE	Okamura, H., Tsuchi, H., Komatsu, T., Yutsudo, M., Hakura, A., Tanimoto, T., Toriige, K., Okura, Y., Nakada, Y., Hattori, K., Akita, K., Nambe, M., Tanabe, F., Konishi, K., Fukuda, S. and Kurimoto, M.		
JOURNAL	Cloning of a new cytokine that induces IFN-gamma production by T cells		
MEDLINE	Nature 378: (6552), 88-91 (1995)		
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	/db_xref="taxon:10090"		

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/translation="MAAISEDSCVNFKEMFIDNTLYPIEENGDESDFRLHCTT
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SKMSYLSCKNKIISFEEDPPEPIDIOSDLFFOKRVPGHNMKEFESSLYEGHFLAC
OKEDAFKILKKDENGDKSVFTLTNLHOS"
866

polyA_site 262 a 187 c 187 g 230 t
BASE COUNT
ORIGIN

Query Match 99.9%; Score 470.6; DB 12; Length 866;
Best Local Similarity 99.8%; Pred. No. 1.3e-103;
Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTGGCCGACTTCACTGTACACCGCAGTATACGGATTAATATGACCAAGTTCTC 60
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DB 270 AACTTGGCCGACTTCACTGTACACCGCAGTATACGGATTAATATGACCAAGTTCTC 329
OY 61 TTGCTGACAAAAGACAGCGCTGTGTCGAGATATGACTGATATGATCAAGTGCAGT 120
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DB 330 TTGCTGACAAAAGACAGCGCTGTGTCGAGATATGACTGATATGATCAAGTGCAGT 389
OY 121 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGTAAAGAGTGGCT 180
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DB 390 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGTAAAGAGTGGCT 449
OY 181 GTGACCCCTCTGTGTAAGGATTAATAAAGTACCCCTCTCTGTAAGAACAGATCAT 240
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DB 450 GTGACCCCTCTGTGTAAGGATTAATAAAGTACCCCTCTCTGTAAGAACAGATCAT 509
OY 241 TCCCTTGAGAAATGATCCACCTGAAATATGATGATATACAAAGTATCATATTTC 300
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DB 510 TCCCTTGAGAAATGATCCACCTGAAATATGATGATATACAAAGTATCATATTTC 569
OY 301 TTTCAGAAACGTGTCAGAGACACAACAGATGAGTTGAAATCTTCACATGTAGAAGA 360
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DB 570 TTTCAGAAACGTGTCAGAGACACAACAGATGAGTTGAAATCTTCACATGTAGAAGA 629
OY 361 CACTTCTGCTTGCCAAAAGAGATGATGCTTCAACTCTTCTGAAAAAAGAGAT 420
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DB 630 CACTTCTGCTTGCCAAAAGAGATGATGCTTCAACTCTTCTGAAAAAAGAGAT 689
OY 421 GAAATAGGGGATTAATCTGTAATGTTCACTCTCACTAATCTTACATCAAACT 471
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DB 690 GAAATAGGGGATTAATCTGTAATGTTCACTCTCACTAATCTTACATCAAACT 740

RESULT 10
MM066244 572 bp MRNA ROD 18-MAR-1997
LOCUS
DEFINITION Mus musculus interferon-gamma inducing factor mRNA, partial cds.
ACCESSION U66244
VERSION U66244.1 GI:1561735
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Active stage of autoimmune diabetes is associated with the
JOURNAL expression of a novel cytokine, IGIF, which is located near Idd2
MEDLINE 3. Clin. Invest. 99 (3), 469-474 (1997).
97174346
REFERENCE 2 (bases 1 to 572)
AUTHORS Rothe, H., Copeland, N.G. and Kolb, H.

TITLE Direct Submission
JOURNAL Submitted (06-AUG-1996) Diabetes Research Institute, Aufm
Hennekamp 65, Duesseidorf 40225, Germany
FEATURES
source
1..572
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/strain="non obese diabetic (NOD)"
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/chromosome="9"
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BASE COUNT 196 a 111 c 113 g 152 t
ORIGIN

Query Match 96.0%; Score 452; DB 12; Length 572;
Best Local Similarity 98.9%; Pred. No. 3.9e-99;
Matches 465; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

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DB 106 AACTTGGCCGACTTCACTGTACACCGCAGTATACGGATTAATATGACCAAGTTCTC 165
OY 61 TTGCTGACAAAAGACAGCGCTGTGTCGAGATATGACTGATATGATCAAGTGCAGT 120
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DB 166 TTGCTGACAAAAGACAGCGCTGTGTCGAGATATGACTGATATGATCAAGTGCAGT 225
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DB 226 GAACCCAGACAGCAGTATATATACATGTACAAAGACAGTAAAGTAAAGAGTGGCT 285
OY 181 GTGACCCCTCTGTGTAAGGATTAATAAAGTACCCCTCTCTGTAAGAACAGATCAT 240
|||||
DB 286 GTGACCCCTCTGTGTAAGGATTAATAAAGTACCCCTCTCTGTAAGAACAGATCAT 345
OY 241 TCCCTTGAGAAATGATCCACCTGAAATATGATGATATACAAAGTATCATATTTC 300
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DB 346 TCCCTTGAGAAATGATCCACCTGAAATATGATGATATACAAAGTATCATATTTC 405
OY 301 TTTCAGAAACGTGTCAGAGACACAACAGATGAGTTGAAATCTTCACATGTAGAAGA 360
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OY 421 GAAATAGGGGATTAATCTGTAATGTTCACTCTCACTAATCTTACATCAAACT 470
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DB 526 GAAATAGGGGATTAATCTGTAATGTTCACTCTCACTAATCTTACATCAAACT 572

RESULT 11
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LOCUS
DEFINITION Rattus norvegicus interferon-gamma inducing factor precursor (IGIF)
ACCESSION U77776
VERSION U77776.1 GI:1809128
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

QY	2	ACTTGGGCGACCTTCACTGATACACCGCGATATCGGAATTAATGACCAAGTCTCT	61
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QY	179	CTGTGACCCCTCTGTGTGAAGGATAGTAAAAATGTACCCCTCTCTGTAAAGAACAAAGATCA	238
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QY	239	TTTCTCTTGAGAGAAATGATCCACTGAAATATTTGATGATATACAAAGTATCTCATAT	298
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QY	299	TCTTTCAGAAACGTGTTCCAGACACCAACCAAGATGAGTTGGAATCTTCACGTGTGAG	358
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QY	359	GACACTTTCTTGTCTGCCAAAGGAAGATGATGCTTCAAACTCATCTTGAAAAAAGAG	418
Db	470	GACACTTTCTTGTCTGCCAAAGGAAGATGATGCTTCAAACTCATCTTGAAAAAGAGAG	529
QY	419	ATGAAATGGGATAAATCTGTAATGTCCACTCCACATCACTTAATTAATTAAGT	471
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QY	62	TGCGTTGACAAAAGA---CAGCGCTGTGTCCGAGGATATCACTGATATTGTACAAAGTGCA	118
Db	170	TGCGTTGACAAAAGAAACCCGCGCTGTGTTCGAGAGCATGCCCTGATATCGACCGACGACGCA	229
QY	119	GTGAAACCCAGACAGACTATATATATCATGTACAAAGACAGTGAAGTAAGAGACTGG	178
Db	230	ACGATATCCCAACCCAGACTGATATATATATATATGTCAAAAGATGCAAGTAAGAGACTGG	289
QY	179	CTGAGACCCCTCTGTGAGAGATGTGTAAGATGCTTACCCTCTCTGTAAAGCAAGAATCA	238
Db	290	CTGAGACCCCTATCTGTGAAGAGATGGAAGAGTGTACCTCTCTGTAAAGCAAGAATCA	349

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Oy      1 AACTTGGCCGACTTCACTGTACAAACCGCAGTAATACGGAAATATAAATGACCAAGTCTC 60
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2000, 21:13:24 : Search time 39.29 Seconds
(without alignments)
136.636 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NFRHLHCTAVIRINQVVL.....KKDENGKSVMTLNLHOS 157

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	806	99.8	157	R99559	Mouse mature inter
2	806	99.8	157	R92506	Interferon gamma p
3	806	99.8	157	W15704	Mouse interferon-g
4	806	99.8	157	W24262	Murine protein for
5	806	99.8	157	W77078	Mouse interleukin
6	806	99.8	157	W77159	Murine interleukin
7	806	99.8	157	W63811	Mouse IL-18 protei
8	806	99.8	157	Y39800	Interleukin-18 rec
9	806	99.8	157	Y44598	Mouse monomeric in
10	806	99.8	157	Y53905	Amino acid sequenc
11	806	99.8	157	Y57571	Murine interleukin
12	806	99.8	180	W48960	Wild-type mouse in

13	797	98.6	157	W77090	Mouse interleukin
14	797	98.5	157	W48968	Mutant mouse inter
15	796	98.5	157	W77091	Mouse interleukin
16	796	98.5	157	W48969	Mutant mouse inter
17	736.5	91.2	194	W53282	Amino acid sequenc
18	6251	77.4	193	Y58241	Equine interleukin
19	538	66.6	157	W77084	Human interleukin
20	524	64.9	157	W48962	Mutant human inter
21	524	64.9	157	W77083	Human interleukin
22	521	64.5	157	W48961	Mutant human inter
23	521	64.5	157	W77077	Human interleukin
24	518	64.1	157	Y57570	Human interleukin
25	518	64.1	158	W85167	Human interleukin
26	518	64.1	180	W48959	Wild-type human in
27	518	64.1	193	W22047	Interferon gamma i
28	518	64.1	193	W46582	Amino acid sequenc
29	515	63.7	157	W77080	Human interleukin
30	515	63.7	157	W77088	Human interleukin
31	515	63.7	157	W48966	Mutant human inter
32	515	63.7	157	W77082	Interleukin 18 act
33	515	63.7	193	W77086	Human interleukin
34	514	63.6	157	W48964	Mutant human inter
35	514	63.6	157	R99558	Human mature inter
36	513	63.5	157	R99558	Human mature inter
37	513	63.5	157	W15701	Interferon-gamma i
38	513	63.5	157	W24258	Human protein for
39	513	63.5	157	W77158	Human interleukin
40	513	63.5	157	W63810	Human IL-18 protei
41	513	63.5	157	W37741	IFN-gamma inducing
42	513	63.5	157	W52176	Interleukin-gamma i
43	513	63.5	157	Y39799	Interleukin-18 rec
44	513	63.5	157	Y44597	Human interleukin-
45	513	63.5	157		

ALIGNMENTS

RESULT	1
R99559	
ID	R99559 standard; Protein: 157 AA.
XX	
AC	R99559;
XX	
DT	29-SEP-1996 (first entry)
XX	
DE	Mouse mature interferon-gamma inducer protein.
XX	
KW	Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW	antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
KW	therapy; cancer.
XX	
OS	Mus sp.
XX	
FT	Key
FT	Misc-difference 70
FT	Location/Qualifiers
XX	/label=11e,Thr
XX	
PN	EP712931-A2
XX	
PD	22-MAY-1996
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PF	95EP-0308055
XX	
PR	10-NOV-1995;
XX	
PR	29-SEP-1995;
XX	
PR	15-NOV-1994;
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PR	23-FEB-1995;
XX	
PR	10-MAR-1995;
XX	
PR	18-SEP-1995;
XX	
PA	(HAYB) HAYASHIBARA SEIBOTSU KAGAKU.
XX	
PI	Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;

PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 XX
 DR MPI: 1996-252837/26.
 DR N-PSDB: T32403.
 XX
 XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Example A-3-2; Page 36-37; 48pp; English.
 XX
 CC A novel mouse protein (R99559) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 XX
 SO Sequence 157 AA:

Query Match 99.8%; Score 806; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NEGRHCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQRLIIMYKDEVRGIA 60
 DB 1 ngrhctavirndqylfvdkrqpvedmtdidqasapqrlilimykdevrigia 60
 OY 61 VTLVKDSKXSTLSCKNKLIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFESSLYEG 120
 DB 61 vtlvksdskxstlscknkliisfeemdpennididsdliffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafkllkkkdehgdksvmftltnlhqs 157

RESULT 2
 R92506
 ID R92506 standard; Protein; 157 AA.
 XX
 AC R92506;
 XX
 DT 02-SEP-1996 (first entry)
 XX
 DE Interferon gamma production inducer protein.
 XX
 KW Interferon gamma; inducer; IFNgamma; immunocompetent cell; antiviral;
 KW antitumour; antiseptic; immunoregulatory; platelet-increasing agent;
 KW therapy; prevention; condyoma acuminatum; renal cancer; brain cancer;
 KW granuloma; mycosis fungoides; rheumatism; allergy; cytotoxicity; AIDS;
 KW killer T-cell; interleukin-2; IL-2; tumour necrosis factor; TNF;
 KW adoptive immunotherapy; monoclonal antibody.
 KW
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70
 FT /label= Met, Thr
 XX
 XX EP692536-A2.
 XX
 XX 17-JAN-1996.
 XX
 XX 13-JUL-1995; 95EP-0304906.
 XX
 XX 10-FEB-1995; 95JP-0045057.
 XX
 XX 14-JUL-1994; 94JP-0184162.
 XX
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 XX Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M;

PI Tanimoto T, Torigoe K;
 XX
 DR MPI: 1996-070177/08.
 DR N-PSDB: T92506.
 XX
 XX Protein that induces gamma interferon prodn. in immuno:competent
 PT cells - used e.g. as antiviral or antitumour agent, also induces
 PT cytotoxicity of killer cells
 XX
 PS Claim 2; Page 22; 30pp; English.
 XX
 CC This sequence represents the interferon gamma (IFNgamma) inducer protein
 CC of the invention. This protein induces IFNgamma production in
 CC immunocompetent cells. The protein is useful as an antiviral,
 CC antitumour, antiseptic, immunoregulatory and platelet-increasing agent.
 CC It can be used for treating or preventing AIDS, condyoma acuminatum,
 CC renal or brain cancer, granuloma, mycosis fungoides, rheumatism and
 CC allergy. The protein can also be used to induce IFNgamma production in
 CC cultured cells. The IFNgamma inducer strongly induces cytotoxicity of
 CC killer T-cells and when used with interleukin-2 (IL-2) and tumour
 CC necrosis factor (TNF), may improve the effect (or reduce side effects) of
 CC adoptive immunotherapy in tumours. The DNA encoding this sequence can
 CC be used to produce the protein, which can then be purified (or assayed)
 CC using monoclonal antibodies.
 XX
 SO Sequence 157 AA:

Query Match 99.8%; Score 806; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NEGRHCTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQRLIIMYKDEVRGIA 60
 DB 1 ngrhctavirndqylfvdkrqpvedmtdidqasapqrlilimykdevrigia 60
 OY 61 VTLVKDSKXSTLSCKNKLIISFEEMDPENIDIOSDLIFQKRVPGHNKMEFESSLYEG 120
 DB 61 vtlvksdskxstlscknkliisfeemdpennididsdliffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafkllkkkdehgdksvmftltnlhqs 157

RESULT 3
 W15704
 ID W15704 standard; peptide; 157 AA.
 XX
 AC W15704;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Mouse interferon-gamma inducer protein.
 XX
 KW Interferon-gamma, IFN-gamma; antiviral; antitumour; radiotherapy;
 KW immunoregulatory; antitumour agent; chemotherapy; leukaemia;
 KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 KW
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70
 FT /label= Met, Thr
 XX
 XX EP767178-A1.
 XX
 XX 09-APR-1997.
 XX
 XX 26-SEP-1996; 96EP-0306997.
 XX
 XX 20-SEP-1996; 96JP-0269105.

PR 26-SEP-1995; 95JP-0270725.
PR 29-FEB-1996; 96JP-0067434.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
XX WPI: 1997-205381/19.
DR N-PSDB: T60536.
XX
PT Human protein that induces interferon-gamma prodn. in
PT immuno:competent cells - useful for adoptive immuno:therapy of
PT tumours and as antimicrobial agent etc.
XX
PS Disclosure: Page 22; 26pp; English.
XX
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antitumor agent for antitumor
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hayfever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukopenia and thrombocytopenia associated with
CC radiotherapy or chemotherapy of leukaemia and other cancers. When used
CC in antitumor immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2), compared with use
CC of IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC (intended for return to the patient) are being grown.
XX
SQ Sequence 157 AA;

Query Match 99.8%; Score 806; DB 18; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NEGRHCTTAVIRININDOVLFVDRKQPFEDMTDIDOSASEPOTRLIITYMKDSEVRGLA 60
DB 1 ngrhcttavrinnndqylfvdkrqpfdemtdidgsasepqrllllymkdsevrsla 60
QY 61 VLSYKDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFQKRVPGHNMKEFESSLYEG 120
DB 61 vlsykdskxstlscknkisfeemdpennididgsdlifqkrvpgnhnmkefesslyeg 120
QY 121 HFLACQKEDDAFKLILKKKDKSGKSVFTLTNLHOS 157
DB 121 hflacqkeddafklllkkkdksgksvmftltlnhqs 157

RESULT 4
ID W24262 standard; Protein; 157 AA.
XX
AC W24262;
XX
DT 15-OCT-1997 (first entry)
XX
DE Murine protein for induction of interferon-gamma.
XX
KW Interferon-gamma; immunocompetent cell; malignant tumour;
KW viral disease; bacterial infection; immune disease.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 70 /note= "Encoded by AYT"
XX
PN JP09157180-A.
XX
PD 17-JUN-1997.

XX
PE 24-JAN-1996; 96JP-0028722.
XX
PR 04-OCT-1995; 95JP-0279906.
PR 10-MAR-1995; 95JP-0078357.
PR 29-SEP-1995; 95JP-0274968.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
DR WPI: 1997-369391/34.
DR N-PSDB: T80210.
XX
PT A drug containing a polypeptide which induces interferon-gamma -
PT useful for treating e.g. malignant tumours, viral, bacterial or
PT immune diseases
XX
PS Disclosure: Page 10-11; 12pp; Japanese.
XX
CC This sequence represents a protein which induces interferon-gamma
CC production in immunocompetent cells. This protein may be used as
CC the major component in a drug for the prevention and treatment of
CC e.g. malignant tumours, viral diseases, bacterial infections and
CC immune diseases.
XX
SQ Sequence 157 AA;

Query Match 99.8%; Score 806; DB 18; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NEGRHCTTAVIRININDOVLFVDRKQPFEDMTDIDOSASEPOTRLIITYMKDSEVRGLA 60
DB 1 ngrhcttavrinnndqylfvdkrqpfdemtdidgsasepqrllllymkdsevrsla 60
QY 61 VLSYKDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFQKRVPGHNMKEFESSLYEG 120
DB 61 vlsykdskxstlscknkisfeemdpennididgsdlifqkrvpgnhnmkefesslyeg 120
QY 121 HFLACQKEDDAFKLILKKKDKSGKSVFTLTNLHOS 157
DB 121 hflacqkeddafklllkkkdksgksvmftltlnhqs 157

RESULT 5
ID W77078 standard; Protein; 157 AA.
XX
AC W77078;
XX
DT 14-DEC-1998 (first entry)
XX
DE Mouse interleukin 18 protein.
XX
KW Mouse; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
XX
OS Mus sp.
XX
PN EP81663-A2.
XX
PD 02-SEP-1998.
XX
PE 24-FEB-1998; 98EP-0301352.
XX
PR 25-FEB-1997; 97JP-0055468.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX
DR WPI: 1998-448964/39.

DR N-PSDB; V48227.
 XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PS osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 XX primary hyperthyroidism and osteoporosis
 PS Claim 6; Page 19; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 6.2e-79;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NFGRLHCTTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQTRLIIYMKDSEVRGLA 60
 ID 1 nfgrlhcttavrindqvlfvdkrqpvedmtidqasasepqrlliiymkdsevrqsla 60
 QY 61 VTLTVSKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFPQKRVPGHNKMEFESSLYEG 120
 DB 61 vtltsvksksxstlscnknkistfeemdpennididqsliffqkrvpgnkmefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTLNHS 157
 DB 121 hflacqkedaafklilkkkdeengdksvmftltnlqhs 157
 RESULT 6
 ID W77159 standard; Protein; 157 AA.
 AC W77159;
 XX
 ID 26-NOV-1998 (first entry)
 XX
 DE Murine interleukin-18 protein (IL-18)
 XX
 KM Murine; interleukin-18 receptor; IL-18; cytokine; signal transduction;
 KM immune system; treatment; autoimmune; allergic disease;
 KW immunosuppressant.
 OS
 XX Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 70 /note="Met or Thr"
 FT
 XX EP864585-A1.
 PN
 PD 16-SEP-1998.
 XX
 PF 23-DEC-1997; 97EP-0310517.
 XX
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.
 PR 28-JUL-1997; 97JP-0215488.
 XX
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okura T, Torigoe K;
 XX
 DR WPI; 1998-469188/41.
 XX
 PT Interleukin-18 receptor polypeptide(s) - and corresponding DNA,

PT which peptide compounds are useful for treating auto-immune or
 PT allergic diseases
 XX
 PS Disclosure; Page 42; 51pp; English.
 XX
 CC The present sequence represents a murine interleukin-18 (IL-18)
 CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal
 CC transduction in immune systems. The interleukin-18 receptor polypeptide
 CC can be used to neutralise interleukin-18 activity or to treat
 CC interleukin-18 receptor susceptible diseases, especially to treat
 CC autoimmune or allergic diseases or as an immunosuppressant. Conditions
 CC which may be treated include e.g. graft or organ rejection, pernicious
 CC anaemia, insulin-related diabetes, discoid lupus erythematosus,
 CC ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
 CC scleroderma, polymyositis, leukaemia, rheumatoid arthritis, HIV
 CC infections, asthma, atopic dermatitis, and pollinosis. The products may
 CC also be useful in the treatment of septic shock associated with
 CC IFN-alpha.
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NFGRLHCTTAVIRNINDQVLFVDRKQPVFEDMTDIDQASAPQTRLIIYMKDSEVRGLA 60
 DB 1 nfgrlhcttavrindqvlfvdkrqpvedmtidqasasepqrlliiymkdsevrqsla 60
 QY 61 VTLTVSKSKXSTLSCKNKIISFEEMDPENIDIDQSLIFPQKRVPGHNKMEFESSLYEG 120
 DB 61 vtltsvksksxstlscnknkistfeemdpennididqsliffqkrvpgnkmefesslyeg 120
 QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTLNHS 157
 DB 121 hflacqkedaafklilkkkdeengdksvmftltnlqhs 157
 RESULT 7
 ID W63811 standard; Protein; 157 AA.
 AC W63811;
 XX
 ID 28-SEP-1998 (first entry)
 XX
 DE Mouse IL-18 protein fragment.
 XX
 KM Mouse IL-18 protein fragment.
 KM Interleukin-18; IL-18; murine; treatment; autoimmune disease; antibody;
 KW immunosuppressant; inhibitor; receptor protein; detection.
 OS
 XX Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..157
 FT /label= IL-18
 FT /note="partial sequence"
 FT Misc-difference 69 /label= Met or Thr
 FT
 XX EP850952-A1.
 PN
 PD 01-JUL-1998.
 XX
 PF 23-DEC-1997; 97EP-0310555.
 XX
 PR 28-JUL-1997; 97JP-0215490.
 PR 26-DEC-1996; 96JP-0356426.
 PR 21-FEB-1997; 97JP-0052526.
 PR 06-JUN-1997; 97JP-0163490.
 XX
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;
 PI MPI: 1998-335317/30.
 XX
 DR
 XX
 PT New interleukin-18 receptor protein used to inhibit interleukin-18,
 PT to treat autoimmune disease and as immunosuppressant - and new
 PT monoclonal antibody and hybridoma used to detect interleukin-18
 PT receptor protein
 XX
 PS Claim 5; Page 16-17; 35pp; English.
 XX
 CC This sequence represents a mouse interleukin-18 (IL-18) fragment which is
 CC used in a method involved in neutralising IL-18 or to treat autoimmune
 CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
 CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
 CC receptor protein (labeled with an enzyme or a radioactive or fluorescent
 CC substance). The protein is used to treat e.g. graft rejection, pernicious
 CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
 CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
 CC cold-agglutinin-related diseases, Goodpasture's syndrome, primary
 CC biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile
 CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
 CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
 CC lupus erythematosus, polyleptic cold haemaglobinuria, polymyositis,
 CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
 CC haemorrhagica, Basedow's disease, leukopenia, Behcet's disease,
 CC climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic
 CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
 CC nasitis, pollinosis, aptoxin allergy and septic shock resulting from
 CC production or administration of excessive gamma interferon (IFN-gamma).
 CC
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINNDQVLFVDKROPVFEDMDIDQASSEPQRLIIYWKSEVGLA 60
 DB 1 nfgrlhcttavrindqvlfvdkrpvfedmdidqassepqrliliiymkxsevgla 60
 OY 61 VTLISVSKSKSTISCKNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNKMEFESSLYEG 120
 DB 61 vtlisvskskstiscknkisifeemdpennididgsdliffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDDNGDKSVMTLTNLHQS 157
 DB 121 hflacqkeddafklllkkkddngdksvmftltnlhqs 157
 RESULT 8
 Y39800 Y39800 standard; Protein: 157 AA.
 XX
 AC Y39800;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Interleukin-18 receptor protein sequence fragment.
 XX
 KM Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
 KM IL-18 receptor sensitive disease; immune reaction; therapy.
 OS Mammalia.
 XX
 XX
 FH Key Location/Qualifiers
 FT Msc-difference 70
 FT /note- "unspecified amino acid"
 XX
 PN JP11240898-A.

PD 07-SEP-1999.
 XX
 XX
 PF 12-MAR-1998; 98JP-0078549.
 XX
 XX
 PR 12-MAR-1997; 97JP-0074697
 PR 28-JUL-1997; 97JP-0215488.
 PR 09-OCT-1997; 97JP-0291837.
 PR 26-DEC-1997; 97JP-0366908.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 DR MPI: 1999-555071/47.
 XX
 PT New polypeptide - useful against interleukin-18 receptor sensitive
 PT diseases
 XX
 PS Disclosure; Page 37-38; 41pp; Japanese.
 XX
 CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
 CC invention. The IL-18R sequences were isolated from human and mouse. The
 CC sequences can be used in drugs for treating IL-18 receptor sensitive
 CC disease, especially effective for the relief of rejection accompanied to
 CC organ transplantation and for the treatment and the prevention of various
 CC diseases caused by excessive immune reaction.
 CC
 XX
 SQ Sequence 157 AA:
 Query Match 99.8%; Score 806; DB 20; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINNDQVLFVDKROPVFEDMDIDQASSEPQRLIIYWKSEVGLA 60
 DB 1 nfgrlhcttavrindqvlfvdkrpvfedmdidqassepqrliliiymkxsevgla 60
 OY 61 VTLISVSKSKSTISCKNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNKMEFESSLYEG 120
 DB 61 vtlisvskskstiscknkisifeemdpennididgsdliffqkrvpgnhkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDDNGDKSVMTLTNLHQS 157
 DB 121 hflacqkeddafklllkkkddngdksvmftltnlhqs 157
 RESULT 9
 Y44598 Y44598 standard; Protein: 157 AA.
 XX
 AC Y44598;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Mouse monomeric interleukin-18.
 XX
 KM Mouse interleukin-18; IL-18; anti-IL-18-antibody; immunopathies;
 KM inflammatory disorder; autoimmune disease; anti-allergic;
 KM anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
 KM antiaplgic; antipyretic.
 XX
 OS Mus musculus.
 XX
 XX
 FH Key Location/Qualifiers
 FT Msc-difference 70
 FT /label= Met, Thr
 XX
 PN EP974600-A2.
 XX
 PD 26-JAN-2000.
 XX
 PF 24-JUN-1999; 99EP-0304977.
 XX
 PR 24-JUN-1998; 98JP-0177580.

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PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX WPI: 2000-118341/11.
XX
XX New artificially produced peptide for neutralizing biological activity
XX of interleukin-18, useful for treating and preventing immunopathies,
XX inflammatory disorders and autoimmune diseases -
XX
XX Disclosure: Page 27; 32pp; English.
XX
XX The present sequence is mouse monomeric interleukin-18. This can comprise
XX a part or the whole of the variable region in anti-interleukin-18
XX -antibody for neutralising interleukin-18. This is useful for treating
XX and preventing immunopathies, inflammatory disorders and autoimmune
XX diseases which are caused by excessive immunoreaction. The protein has
XX anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic,
XX leukocytopenic, antialgic, antipyretic and hepatic-function improving
XX activities.
XX
XX Sequence 157 AA:
SQ

```

Query Match 99.8%; Score 806; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NGRRLHCTTAVIRNINDQVLFVDRKRPVFEEDMTDIDQASSEPQTRLIIYMKDSEVRGLA 60
DB 1 ngrhlcttavrlnndqvlfdvdrkrpvfedmtidqassepqtrliiymkdsevrsla 60
OY 61 VLSVDSKXSTLSCKNKKIISFEEDMPENIDDIQSDLIFFQKRVPGHNKMFESSLYEG 120
DB 61 vlsvdsksxstlscknkliisfeemdpeniddiqsdliiffqkrvpghnkmesfesslyeg 120
OY 121 HFLACOKEDDAFKLILKKKDENGDKSVMTLTNHHOS 157
DB 121 hflacqkeddafklllkkkdengdksvmtltnhbs 157

```

RESULT 10
 Y53905 standard; Protein: 157 AA.
 Y53905;
 13-MAR-2000 (first entry)

Amino acid sequence of a protein that induces IFN-gamma production.
 Mouse; interferon gamma production; IFN-gamma; immunocompetent cell;
 antiviral; immunoregulatory; antigen; mitogen;
 IFN-gamma susceptible disease; antibacterial; herpes syndrome; condyloma;
 AIDS; bacterial disease; candidiasis; malaria; solid malignant tumour;
 renal cancer; mycosis fungoides; chronic granulomatous disease;
 blood cell malignant tumour; adult T cell leukaemia;
 chronic myelogenous leukaemia; malignant leukaemia; immune disease;
 allergy; rheumatism.
 Mus sp.
 Key Location/Qualifiers
 FT Misc-difference 70 /note="unspecified residue encoded by AYC"
 FT
 XX EP962531-A2.
 XX 08-DEC-1999.
 XX PD

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XX 10-NOV-1995; 99EP-0104104.
XX
XX 15-NOV-1994; 94JP-0304203.
XX 23-FEB-1995; 95JP-0058340.
XX 10-MAR-1995; 95JP-0078357.
XX 18-SEP-1995; 95JP-0262062.
XX 29-SEP-1995; 95JP-0274988.
XX 10-NOV-1995; 95EP-0308055.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Ushio S, Torigoe K, Tanimoto T, Okamura H;
XX
XX WPI: 2000-064289/06.
XX N-PSDB: 236923.
XX
XX Novel polypeptides used in the treatment of interferon-gamma
XX susceptible diseases -
XX
XX Disclosure: Page 3; 42pp; English.
XX
XX The present sequence represents a murine protein that induces interferon
XX (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
XX protein which has antiviral, antitumor and immunoregulatory activities,
XX and is produced by immunocompetent cells stimulated with antigens or
XX mitogens. A probe derived from the cDNA of the present sequence was used
XX to isolate the corresponding human protein from human liver cells. The
XX protein of the invention is used to treat IFN-gamma susceptible diseases,
XX and also have use as a antiviral agent, antibacterial agent, antitumor
XX agent, immunoregulatory agent and blood platelet enhancing agent.
XX Diseases which can be treated with the protein include viral diseases
XX such as hepatitis, herpes syndrome, condyloma, and AIDS; bacterial
XX diseases such as candidiasis and malaria; solid malignant tumours such
XX as renal cancer, mycosis fungoides and chronic granulomatous disease;  

XX blood cell malignant tumours such as adult T cell leukaemia, chronic
XX myelogenous leukaemia, and malignant leukaemia; and immune diseases
XX such as allergy and rheumatism.
XX
XX Sequence 157 AA:
SQ

```

Query Match 99.8%; Score 806; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 6.2e-79;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 NGRRLHCTTAVIRNINDQVLFVDRKRPVFEEDMTDIDQASSEPQTRLIIYMKDSEVRGLA 60
DB 1 ngrhlcttavrlnndqvlfdvdrkrpvfedmtidqassepqtrliiymkdsevrsla 60
OY 61 VLSVDSKXSTLSCKNKKIISFEEDMPENIDDIQSDLIFFQKRVPGHNKMFESSLYEG 120
DB 61 vlsvdsksxstlscknkliisfeemdpeniddiqsdliiffqkrvpghnkmesfesslyeg 120
OY 121 HFLACOKEDDAFKLILKKKDENGDKSVMTLTNHHOS 157
DB 121 hflacqkeddafklllkkkdengdksvmtltnhbs 157

```

RESULT 11
 Y57571 standard; protein: 157 AA.
 Y57571;
 06-MAR-2000 (first entry)

Murine interleukin 18 protein sequence SEQ ID NO.2.
 Murine; interleukin 18; IL-18; potentiator; IGF; tumour; cancer;
 interferon-gamma-inducing factor; growth inhibition; cyostatic.
 Mus sp.
 OS

XX MO959565-A1.
XX 25-NOV-1999.
XX 20-MAY-1999; 99WO-US11160.
XX 21-MAY-1998; 98US-0086560.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Johnson RK;
XX WPI: 2000-062368/05.
XX
XX New polypeptides, useful for preparation of composition for preventing
XX and/or treating cancer by inhibiting tumor growth
XX
XX Claim 2; Page 50; 53pp; English.
XX
XX The present sequence represents murine interleukin 18 (IL-18). The
XX present invention describes a compound comprising human or murine IL-18
XX in combination with a chemotherapeutic agent (I). Also described are:
XX (1) a method of preventing and/or treating cancer in a mammal comprising
XX the administration of a cancer inhibiting amount of (I) comprising the
XX IL-18 protein and the chemotherapeutic agent and optionally a
XX pharmaceutically acceptable carrier; and (2) a method of inhibiting the
XX growth of tumor cells in a mammal sensitive to a composition comprising
XX human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
XX optionally a pharmaceutically acceptable carrier), comprising
XX administering to a mammal afflicted with the tumor cells an effective
XX amount of growth inhibiting amount of (I). The IL-18 protein in
XX conjunction with a chemotherapeutic agent is useful in a method for
XX preventing and/or treating cancer in mammals by inhibiting the growth
XX of tumours or cancerous cells in mammals.
XX
XX Sequence 157 AA;
SQ
Query Match 99.8%; Score 806; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 6.2e-79;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 NFGRLHCTTAVIRININDVLFVDRKQPFEDMTDIDQASBPORLIIYWKDSEVGIA 60
Db 1 nfgrlhcttavrlnindqlvdrkqpfeomtdidqasbpqtrlllymkdsevgia 60
OY 61 VTLGVKDSKXSTLCKNKKIISFEEMDPENIDIQSDLIFFQKRVPGHNKMEFESSLYEG 120
Db 61 vtlsvkdsksmtlscnkklisfeemdpennididqsdliiffqkrvpghnmkfesslyeg 120
OY 121 HFLACQKEDDAFKLILKKKDKGSKSVWFTLTNHHOS 157
Db 121 hflacqkeddafklllkkkdkngsksvwftltlnhgs 157
RESULT 12
W48860
ID W48960 standard; Peptide; 180 AA.
XX
XX W48960;
AC
XX
XX 25-SEP-1998 (first entry)
DT
XX
XX Wild-type mouse interferon-gamma inducing factor.
DE
XX
XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
KW antitumor agent; antiviral agent; antimicrobial agent; tumour; mGIF;
KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX
XX Mus sp.
OS
XX

FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note- "Signal peptide"
FT 24..180
FT /note- "Mature mouse IGF which is claimed by the
FT inventors under claim 4 in the specification"
XX
XX EP84530-A2.
PN
XX
XX 03-JUN-1998.
PD
XX
XX 28-NOV-1997; 97EP-0309632.
PE
XX
XX 14-NOV-1997; 97JP-0329715.
PR 29-NOV-1996; 96JP-033037.
PR 21-JAN-1997; 97JP-0020906.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA
XX
XX Kurimoto M, Okamoto I, Yamamoto K;
PI
XX
XX WPI: 1998-288747/26.
DR
XX
XX N-PSDB; V32755.
DR
XX
XX Mutants of interferon-gamma inducing polypeptide - useful as
XX antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX
XX Claim 4; pages 38-39; 59pp; English.
XX
XX The present sequence represents the wild-type mouse interferon-gamma
XX inducing factor (mGIF). The invention provides for mutant human and
XX mouse interferon-gamma inducing factors in which one or more cysteine
XX residues are replaced with different residues at or away from the
XX consensus sequences shown in W48956-W48958. The mutant mGIFs are
XX capable of stimulating immunocompetent cells for the production of
XX interferon-gamma and are claimed to be less toxic, more active and stable
XX than the corresponding wild type mGIF. The mutant mGIFs are also
XX claimed to enhance killer cell cytotoxicity and/or induce killer cell
XX formation; and may therefore be useful as antitumour agents, antitumour
XX immunotherapeutics, antiviral agents and antimicrobial agents. The
XX mutant mGIFs are also claimed to be useful for treating hepatitis,
XX acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
XX malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
XX thrombopenia caused by radiation- and chemo-therapy.
XX
XX Sequence 180 AA;
SQ
Query Match 99.8%; Score 806; DB 19; Length 180;
Best Local Similarity 99.4%; Pred. No. 7.5e-79;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 NFGRLHCTTAVIRININDVLFVDRKQPFEDMTDIDQASBPORLIIYWKDSEVGIA 60
Db 24 nfgrlhcttavrlnindqlvdrkqpfeomtdidqasbpqtrlllymkdsevgia 83
OY 61 VTLGVKDSKXSTLCKNKKIISFEEMDPENIDIQSDLIFFQKRVPGHNKMEFESSLYEG 120
Db 84 vtlsvkdsksmtlscnkklisfeemdpennididqsdliiffqkrvpghnmkfesslyeg 143
OY 121 HFLACQKEDDAFKLILKKKDKGSKSVWFTLTNHHOS 157
Db 144 hflacqkeddafklllkkkdkngsksvwftltlnhgs 180
RESULT 13
W77090
ID W77090 standard; Peptide; 157 AA.
XX
XX W77090;
AC
XX
XX 16-NOV-1998 (first entry)
DT
XX

DE Mouse interleukin 18 derivative 1.
 XX
 KW Mouse; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
 XX
 OS Mus sp.
 XX
 PN EP861663-AZ.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI: 1998-448964/39.
 XX
 XX
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis
 PS
 PS Disclosure: Page 34; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 CC
 SO Sequence 157 AA:
 Query Match 98.6%; Score 797; DB 19; Length 157;
 Best Local Similarity 98.7%; Pred. No. 5.7e-78;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINOVLFVDRKQPVFEDMDIDQASSEPQRLITYMYKDSVGRGLA 60
 DB 1 nfgrlhcttavrlnndqvlfdktrqpvfedmdidqgsasepqrlllymykdsavgla 60
 OY 61 VTLVSKDKSKSTLSCKNKIISFEEMDPENIDIDQSDLIFFOKRVPCHNKEFESSLYEG 120
 DB 61 vtlsvdkdkstlsccknkliisfeemdpennididqsdliiffqkrvpghnkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafrklllkkkdehgdksvmftltlnhqs 157
 RESULT 14
 ID W48968 standard; Peptide: 157 AA.
 XX
 AC W48968;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Mutant mouse interferon-gamma inducing factor mIGIF/M0711.
 XX
 KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; mIGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX
 OS Mus sp.
 OS Synthetic.

XX
 EH Key Location/Qualifiers
 FT Misc-difference 7
 FT /note= "changed from Cys in wild-type to Ala in
 FT mutant"
 XX
 PN EP845530-AZ.
 XX
 PD 03-JUN-1998.
 XX
 PF 28-NOV-1997; 97EP-0309632.
 XX
 PR 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0333037.
 PR 21-JAN-1997; 97JP-0020906.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okamoto I, Yamamoto K;
 XX
 DR WPI: 1998-288747/26.
 DR N-PSDB: VJ2632.
 XX
 PT Mutants of interferon-gamma inducing polypeptide - useful as
 PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
 PS
 PS Claim 6; page 44; 59pp; English.
 XX
 CC The present sequence represents the mutant mouse interferon-gamma
 CC inducing factor mIGIF/M0711. The wild-type mouse interferon-gamma
 CC factor (mIGIF) sequence is shown in W48960. The invention provides for
 CC mutant human and mouse interferon-gamma inducing factors in which one
 CC or more cysteine residues are replaced with different residues at or away
 CC from the consensus sequences shown in W48956-W48958. The mutant mIGIFs
 CC are capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and stable
 CC than the corresponding wild type mIGIF. The mutant mIGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant mIGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.
 CC
 SO Sequence 157 AA:
 Query Match 98.6%; Score 797; DB 19; Length 157;
 Best Local Similarity 98.7%; Pred. No. 5.7e-78;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NFGRLHCTTAVIRINNDQVLFDKTRQPVFEDMDIDQASSEPQRLITYMYKDSVGRGLA 60
 DB 1 nfgrlhcttavrlnndqvlfdktrqpvfedmdidqgsasepqrlllymykdsavgla 60
 OY 61 VTLVSKDKSKSTLSCKNKIISFEEMDPENIDIDQSDLIFFOKRVPCHNKEFESSLYEG 120
 DB 61 vtlsvdkdkstlsccknkliisfeemdpennididqsdliiffqkrvpghnkmeffesslyeg 120
 OY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
 DB 121 hflacqkedafrklllkkkdehgdksvmftltlnhqs 157
 RESULT 15
 ID W77091 standard; Peptide: 157 AA.
 XX
 AC W77091;
 XX
 DT 16-NOV-1998 (first entry)
 XX

DE Mouse Interleukin 18 derivative 2.

XX
KM Mouse: Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX Chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.
XX

OS Mus sp.

PN EP861663-A2.

PD 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

DR Use of Interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
XX primary hyperthyroidism and osteoporosis

PS Disclosure; Page 34-35; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.

XX Sequence 157 AA;

Query Match

98.58; Score 796; DB 19; Length 157;

Best Local Similarity 98.7%; Pred. No. 7.3e-78;

Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NFGRLHCTTAVIRNINOVLFVDRKQPFEDMTDIDOSASEPOTRLIIVYWKDSEVGLA 60

Db 1 nfgrlhcttaviirindvlfvdkrqpfedmtidqasepqtllilymkdsevirgla 60

OY 61 VTLVKDSKXSTLSCKNKIISFEEMDPENIDIQSDLIFFQKRVPGHNKMEFESSLYEG 120

Db 61 vtlsvkdsksmtlscnkkiisfeemdpennididqsdliifqkrvpghnmkfesslyeg 120

OY 121 HFLACQKEDDAFKLILKKKDENGSKSVMTLTJNLHQS 157

Db 121 hflasqkeddafkllkkkdengdksvmftltlnhqs 157

Search completed: November 21, 2000, 23:16:17
Job time: 7373 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2000, 21:29:19 : Search time 25.82 seconds

(Without alignments)
101.917 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NGRHCTTAVIRININDVL.....KKDENGDKSVMTLTLNHS 157Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/prodata/2/1aa/5A-COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6-COMB.pep:*
4: /cgn2_6/prodata/2/1aa/PCTUS-COMB.pep:*
5: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806	99.8	157	2	US-08-502-535B-2
2	806	99.8	157	2	US-08-908-005A-12
3	806	99.8	157	3	US-08-996-338-27
4	513	63.5	157	2	US-08-896-605A-6
5	513	63.5	157	2	US-08-896-501A-14
6	513	63.5	157	3	US-08-884-324-1
7	513	63.5	157	3	US-08-896-338-26
8	513	63.5	193	2	US-08-896-605A-2
9	513	63.5	193	2	US-08-896-501A-2
10	80.5	10.0	456	1	US-08-464-164-2
11	80.5	10.0	456	1	US-08-338-057-2
12	80.5	10.0	456	2	US-08-668-416-2
13	76.5	9.5	1284	2	US-08-819-288-3
14	76.5	9.5	1321	1	US-08-261-822A-3
15	76.5	9.5	1321	4	PCT-US95-07744A-3
16	75.5	9.3	156	1	US-07-766-682A-3
17	74	9.2	269	1	US-08-203-716-3
18	74	9.2	269	1	US-08-440-179-3
19	74	9.2	269	2	US-08-432-693-11
20	74	9.2	269	2	US-08-489-895-11
21	74	9.2	269	2	US-08-483-806-2
22	74	9.2	269	3	US-09-211-290-11
23	74	9.2	269	3	US-09-030-613-11
24	74	9.2	269	3	US-09-322-676-11
25	74	9.2	269	4	PCT-US91-02339-1
26	74	9.2	1082	1	US-08-106-493A-2
27	74	9.2	1082	1	US-08-429-264-2
28	74	9.2	1139	1	US-08-832-883-2

29	74	9.2	1139	2	US-08-832-877-2	Sequence 2, Appl1
30	71.5	8.8	99	2	US-08-710-749-9	Sequence 9, Appl1
31	71	8.8	65	1	US-08-426-819A-33	Sequence 33, Appl1
32	71	8.8	248	1	US-08-426-819A-37	Sequence 37, Appl1
33	71	8.8	267	5	5494663-5	Patent No. 5494663
34	71	8.8	584	1	US-08-426-819A-36	Sequence 36, Appl1
35	71	8.8	622	1	US-08-426-819A-35	Sequence 35, Appl1
36	71	8.8	628	3	US-08-776-271-2	Sequence 2, Appl1
37	68.5	8.5	2509	1	US-08-469-005A-10	Sequence 10, Appl1
38	68	8.4	155	5	5494663-8	Patent No. 5494663
39	68	8.4	270	2	US-08-611-880-1	Sequence 1, Appl1
40	67.5	8.4	516	2	US-09-019-201A-3	Sequence 1, Appl1
41	67.5	8.4	866	1	US-08-100-692-1	Sequence 1, Appl1
42	67.5	8.4	866	2	US-08-674-030-1	Sequence 1, Appl1
43	67.5	8.4	874	2	US-08-247-904B-8	Sequence 8, Appl1
44	67.5	8.4	874	3	US-08-767-942A-21	Sequence 21, Appl1
45	67	8.3	153	5	5217714-4	Patent No. 5217714

ALIGNMENTS

RESULT 1
US-08-502-535B-2
Sequence 2, Application US/08502535B
Patent No. 591324
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakui
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-502-535B-2

Query Match 99.8% Score 806; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
DB 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
QY 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120
DB 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120

QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157
DB 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157

RESULT 2

US-08-908-005A-2
Sequence 2, Application US/08908005A

Patent No. 5914253

GENERAL INFORMATION:

APPLICANT: OKAMURA, Haruki

APPLICANT: TANIMOTO, Tadao

APPLICANT: TORIGOE, Kakuji

APPLICANT: KUNIKATA, Toshio

APPLICANT: TANIGUCHI, Mutsuko

APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND

TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,005A

FILING DATE: 11-AUG-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/502,535

FILING DATE: 14-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 184162/1994

FILING DATE: 14-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 45057/1995

FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKAMURA-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-908-005A-2

Query Match 99.8% Score 806; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
DB 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
QY 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120
DB 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120

QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157
DB 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157

RESULT 3

US-08-996-338-27
Sequence 27, Application US/08996338

Patent No. 6087116

GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji

APPLICANT: OKURA, Takao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,338

FILING DATE: 22-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74,697/1997

FILING DATE: 12-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 215,488/1997

FILING DATE: 28-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 291,837/1997

FILING DATE: 09-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TORIGOE-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 157

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-996-338-27

Query Match 99.8% Score 806; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.4e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
DB 1 NGRLLCTTAVIRININDQVLFDKRPVFEEDMTDIDQASSEPOTRLIITYMKDSEVRGLA 60
QY 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120
DB 61 VLTSLVSDSKXSTLSCKNKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEESSLYEG 120

QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157
DB 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHOS 157

RESULT

US-08-996-338-27
Sequence 27, Application US/08996338

Patent No. 6087116

GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji

APPLICANT: OKURA, Takao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,338

FILING DATE: 22-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74,697/1997

FILING DATE: 12-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 215,488/1997

FILING DATE: 28-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 291,837/1997

FILING DATE: 09-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TORIGOE-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 157

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-996-338-27

QY 1 NFGRLHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
DB 1 NFGRLHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
QY 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 120
DB 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 120
QY 121 HFLACOKEDDAFLKLLKKDENGDKSVMTFTLNHOS 157
DB 121 HFLACOKEDDAFLKLLKKDENGDKSVMTFTLNHOS 157

RESULT 4
US-08-896-605A-6

Sequence 6, Application US/08896605A
Patent No. 58/9942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-6

Query Match 63.5% Score 513; DB 2; Length 157;
Best Local Similarity 64.9% Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;

QY 2 FGRHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
DB 2 FGRHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
QY 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
DB 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
QY 120 GHFLACOKEDDAFLKLLKKDENGDKSVMTFTLN 153
DB 120 GHFLACOKEDDAFLKLLKKDENGDKSVMTFTLN 153

DB 122 GYFLACOKEDDAFLKLLKKDELDGDSIMFTVON 155

RESULT 5

US-08-896-501A-4
Sequence 4, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 63.5% Score 513; DB 2; Length 157;
Best Local Similarity 64.9% Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;

QY 2 FGRHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
DB 2 FGRHCTAVIRININDOVLFPVDRQPVEDMTDIDQASSEPOTRLIIYMYKDSVYRGIA 60
QY 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
DB 61 VTLVSVDKSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
QY 120 GHFLACOKEDDAFLKLLKKDENGDKSVMTFTLN 153
DB 120 GHFLACOKEDDAFLKLLKKDENGDKSVMTFTLN 153

RESULT 6
US-08-884-324-1
Sequence 1, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:

APPLICANT: Takanori OKURA
APPLICANT: Kakui TORIGOE
APPLICANT: Masashi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
NUMBER OF SEQUENCES: 35
OF INDUCING THE PRODUCTION OF INTERFERON-
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 63.5%; Score 513; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSVGRGA 60
DB 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSVGRGA 60
QY 61 VTLVSKDSKXSTLSCNKKIISFEEDMPENIDDIQSDLIFFOKRVPGH-NKNEFESSLYE 119
DB 62 VTLVSKDSKXSTLSCNKKIISFEEDMPENIDDIQSDLIFFOKRVPGH-NKNEFESSLYE 119
QY 120 GHFLACQKEDDAFKLILKKKDEGDKSVAFETLN 153
DB 122 GYFLACEKERDLFKLILKKKDEGDKSVAFETLN 155

RESULT 7
US-08-996-338-26
Sequence 26, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakui
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 63.5%; Score 513; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 1.6e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSVGRGA 60
DB 2 FGRHCTAVIRINDVLFVDK-RQPVFEDMTDIDQASSEPOTRLIITYMYKDSVGRGA 60
QY 61 VTLVSKDSKXSTLSCNKKIISFEEDMPENIDDIQSDLIFFOKRVPGH-NKNEFESSLYE 119
DB 62 VTLVSKDSKXSTLSCNKKIISFEEDMPENIDDIQSDLIFFOKRVPGH-NKNEFESSLYE 119
QY 120 GHFLACQKEDDAFKLILKKKDEGDKSVAFETLN 153
DB 122 GYFLACEKERDLFKLILKKKDEGDKSVAFETLN 155

RESULT 8
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30

RESULT 9
 US-08-896-501A-2
 Sequence 2, Application US/08896501A
 Patent No. 5891663
 GENERAL INFORMATION:
 APPLICANT: TANIMOTO, Tadao
 APPLICANT: KURIIMOTO, Masashi
 TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/896,501A
 FILING DATE: 18-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 213,267/1996
 FILING DATE: 25-JUL-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 31,474/1997
 FILING DATE: 31-JAN-1997

RESULT 10
 US-08-464-164-2
 Sequence 2, Application US/08464164
 Patent No. 5614195
 GENERAL INFORMATION:
 APPLICANT: Tomley, Fiona M.
 APPLICANT: Dunn, Paul P. J.
 APPLICANT: Bumstead, Janene M.
 APPLICANT: Vermeulen, Arno N.
 TITLE OF INVENTION: Coccidiosis poultry vaccine
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Akzo No. 5614195el Patent Department
 STREET: 1300 Piccard Drive, Suite 206
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464.164
 FILING DATE: June 2, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gormley, Mary E.
 REGISTRATION NUMBER: 34,409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 258-5200
 INFORMATION FOR SEQ. ID NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 456 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-164-2

Query Match 10.0%; Score 80.5; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIITMYKDESEVRGLA---VTLSEKDS-----KXSTLSCKNKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTIDVTAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFKLTKKDENGD 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTITNEETDELNKIIFQKMDKNGD 317

RESULT 11
US-08-338-057-2
Sequence 2, Application US/08338057

PATENT No. 5795741
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338.057
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-057-2

Query Match 10.0%; Score 80.5; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIITMYKDESEVRGLA---VTLSEKDS-----KXSTLSCKNKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTIDVTAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFKLTKKDENGD 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTITNEETDELNKIIFQKMDKNGD 317

RESULT 12

US-08-668-416-2
Sequence 2, Application US/08668416

PATENT No. 5843722
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5843722e1 Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668.416
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/464.164
FILING DATE: June 2, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-416-2

Query Match 10.0%; Score 80.5; DB 2; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.19;
Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

OY 42 POTRLIITMYKDESEVRGLA---VTLSEKDS-----KXSTLSCKNKIISFEENDPPENI 91
DB 216 PQWRKVSSEPAKDLIRKMLAYVPSMRISAKDALDHPWIKSTIDVTAKDSI-----NL 265
OY 92 DDIOSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFKLTKKDENGD 144
DB 266 PSLESTILNT-RQFOGTOKLAALALYMGSKLTITNEETDELNKIIFQKMDKNGD 317

RESULT 13

US-08-619-288-3
Sequence 3, Application US/08819288

PATENT No. 595652
GENERAL INFORMATION:
APPLICANT: Eckert, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 595652-215
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

```
Oy      8 TTAVIRNIND---QVLFD--KRQVEDMTDIDQASSEPQTRLIIYKQSEVRGLAV 61
      ||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    517 TTSVTSVVDLPENILMTDQIRSSPPEERELDVKYSTQ---VSSLKEDSDVKESQSV 578
```

Wed Nov 22 11:24:56 2000

us-09-050-249-2.ra1

Page 8

OY 62 TLS--VKDSKXSTLSCNNKIISEENDPENIDDIQSDFIFQKRVPG 107
DB 572 LOSTVNEVSODKDLIVETMAKIEPMSPEKIVSMENNSKFIEKDYEG 619

Search completed: November 21, 2000, 23:16:55
Job time: 6456 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:31:49 ; Search time 42.57 Seconds
(without alignments)
234.044 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NGRRLHCTAVIRININDVL.....KKDENGDKSVMTFLTNLHOS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	806	99.8	192	S60226	cytokine IGIF - mo
2	82.5	10.2	803	A64070	endopeptidase Ia (
3	82	10.1	267	JN0724	interleukin-1 beta
4	81	10.0	483	T21327	hypothetical prote
5	80.5	10.0	267	S38373	interleukin-1 beta
6	80	9.9	506	D71461	hypothetical prote
7	79.5	9.8	526	A41698	cell division cont
8	78.5	9.7	1039	E72734	hypothetical prote
9	78	9.7	1196	J01467	toxin, nontoxic co
10	78	9.7	1196	S46430	botulinum neurotox
11	78	9.7	1247	E71616	hypothetical prote
12	77.5	9.6	366	T30457	hypothetical prote
13	77	9.5	266	ICB01B	interleukin-1 beta
14	77	9.5	563	T09378	hypothetical prote
15	76.5	9.5	167	A64401	hypothetical prote
16	76.5	9.5	621	B64546	chaperone and heat
17	76.5	9.5	706	S38168	hypothetical prote
18	76.5	9.5	905	T39572	enzymable protein
19	76.5	9.5	1294	T48349	ELN2 protein - Ara
20	76	9.4	525	T43437	hypothetical prote
21	75.5	9.3	270	ICM51	interleukin-1 alph
22	75.5	9.3	439	C64401	hypothetical prote
23	75.5	9.3	626	T35669	hypothetical ATP/G
24	75.5	9.3	695	T64135	carboxy-terminal p
25	75.5	9.3	866	T06454	probable lipoxigen
26	75	9.3	266	E23010	interleukin-1 beta
27	75	9.3	621	A71961	90kDa chaperone -
28	75	9.3	624	S67382	hypothetical prote
29	75	9.3	1146	E70204	hypothetical prote

30	74.5	9.2	270	1	S10532	interleukin-1 alpha
31	74.5	9.2	661	2	S75005	sensory transducti
32	74	9.2	254	2	E70230	conserved hypotet
33	74	9.2	269	1	ICM11B	interleukin-1 beta
34	74	9.2	318	2	C81447	chemotaxis protein
35	74	9.2	322	2	T48460	MADS-box protein-1
36	74	9.2	438	2	T45041	hypothetical prote
37	74	9.2	1139	2	A49370	E1A-associated cyc
38	73.5	9.1	589	1	C72414	anthranilate synth
39	73.5	9.1	647	2	S61973	hypothetical prote
40	73.5	9.1	680	2	T39858	hypothetical prote
41	73.5	9.1	1146	2	T09112	probable sensor ki
42	73.5	9.1	2077	2	T43991	large tegument pro
43	73.5	9.1	2077	2	T44178	large tegument pro
44	73	9.0	611	2	S8162	translation elonga
45	73	9.0	872	1	P2XRCW	RNA-binding protei

ALIGNMENTS

RESULT 1

S60226
cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tautsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009

A:Accession: S60226

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match 99.88; Score 806; DB 2; Length 192;
Best Local Similarity 99.44; Pred. No. 1.9e-65;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	NGRRLHCTAVIRININDVLFVDRKOPFEDMDIDDSASPPORLLIYWKDSEVGLA 60
DB	36	NGRRLHCTAVIRININDVLFVDRKOPFEDMDIDDSASPPORLLIYWKDSEVGLA 95
QY	61	VTLSSVSKSKSTLSCNKKIISFEEMDPENIDIOSDLIFQKRVPGHKKMFESSLYEG 120
DB	96	VTLSSVSKSKSTLSCNKKIISFEEMDPENIDIOSDLIFQKRVPGHKKMFESSLYEG 155
QY	121	HFLACOKEDDAFKLILKKDKDENGKSVMTFLTNLHOS 157
DB	156	HFLACOKEDDAFKLILKKDKDENGKSVMTFLTNLHOS 192

RESULT 2

A64070
endopeptidase Ia (EC 3.4.21.53) - Haemophilus influenzae (strain Rd KW20)

N:Alternate names: ARP-dependent proteinase 10n; ATP-dependent serine proteinase Ia

N:Contents: adenosinetriphosphatase (EC 3.6.1.3)

C:Species: Haemophilus influenzae

C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 18-Jun-1999

C:Accession: A64070

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

; D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: A64070

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-803 <TIGR>
 A:Cross-references: GB:U3729; GB:L42023; NID:g1573439; PIDN:AAC22121.1; PID:g1573440; T
 C:Comment: This allosteric enzyme catalyzes the hydrolysis of large proteins in the pres
 C:Genetics:
 A:Gene: lon; lon-A
 C:Superfamily: ATP-dependent serine proteinase Ia
 C:Keywords: allosteric regulation; ATP; DNA binding; heat shock; hydrolase; P-loop; ser
 F:135-363/Region: nucleotide-binding motif A (P-loop)
 F:419-424/Region: nucleotide-binding motif B
 F:679/Active site: Ser #status predicted

Query Match 10.2%; Score 82.5; DB 1; Length 803;
 Best Local Similarity 18.9%; Pred. No. 10;
 Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

3 GRHCTTAVIRIND--QVLFVNR-----QVFEDMTDIDQAS-----40
 30 GRAKSIATLEAMNDKQILLVSQREADELEPPEDELFDTGTANTITOLIKLPDPTVKVL 89
 41 -EPOTRIIIMYKDE-----VRGLAVTLVKDSXSTLSCNKIISFE 83
 90 VEQNRKIKSLDGEKCFSAQITPIETTYGDEKELVAKSAVLSFENLILNKKVPID 149
 84 EMPDENIDDI-----OSDLIFFOK 103
 150 ILNQLRIDVDRLADTMAHLFVIRKONALELANVQERLEYLGLMSESDIIOVER 209
 104 RVPHNKMFEESLYEGHFLACQEDAFLLIKKDNENDKSVMTLLNHO 156
 210 RIRGRVKKOMERS-QRNYVL-----NEQIKAIRKMDGGENEDTIDEVQLHQ 256

RESULT 3
 JN0724
 Interleukin-1 beta precursor - pig
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
 C:Accession: JN0724
 R:Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Mollitor, T.W.
 Gene 129, 285-289, 1993
 A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be
 A:Reference number: JN0724; MUID:93314975
 A:Accession: JN0724
 A:Molecule type: mRNA
 A:Residues: 1-267 <HUE>
 A:Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608
 A:Experimental source: alveolar macrophage
 C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
 ved form of interleukin-1beta, unlike interleukin-1alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
 C:Superfamily: interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
 F:115-267/Product: Interleukin-1 beta #status predicted
 F:177/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 3.2; Mismatches 31; Indels 12; Gaps 5;
 Matches 23; Conservative 22;

49 YMKDSEVRGLAVTLVKDSXSTLSCNK-----IISFEMDP--PENIDDIOSDLIF 101
 160 FVQGDSDNNKIPVTLGIR-GKNLYLSCVMKNDPTLQLEDIDPKRYPKR--DMERFVFY 216
 102 OKRVPGHNMKEFESSLYEGHFLACQED 129
 217 KTEI--KNRVEFSALYPNWIYSTQAE 242

RESULT 4
 T21327
 hypothetical protein F25C8.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21327
 R:Matthews, L.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19407
 A:Accession: T21327
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <WIL>
 A:Cross-references: EMBL:Z81512; PIDN:CAB04171.1; GSPDB:GN00023; CESP:F25C8.2
 A:Experimental source: clone F25C8
 C:Genetics:
 A:Gene: CESP:F25C8.2
 A:Map position: 5
 A:Introns: 13/2; 136/2; 209/3; 358/3; 444/2

Query Match 10.0%; Score 81; DB 2; Length 483;
 Best Local Similarity 26.4%; Pred. No. 7.8; Mismatches 63; Indels 66; Gaps 12;
 Matches 55; Conservative 24;

3 GRHCTTAVIRINDV-----LFVDRQPVFEDMTDIDQAS-----EPOTRII 48
 81 GTHFGAEYVGVNDVEYNYLVEKYDLF-DKTRKPTDDMLMDQDQNSITLVNGHLVPRKIL 139
 49 YMKDSEVRGLAVTLVKDSXSTLSCNKIIS--FEEN--DPENIDDIOSDLIFFOKRV 105
 140 DKFND-YIRYLVNVALYKESIKINQLSVENEINNOFIEFLRDPVPENDHEIYSLINVKY- 196
 106 PGHNKMEFESSLYEGHFL-----ACQKEDA-----FKLIIL 137
 197 --NYQTWSSPVGLSLSNLSITWDQTEEDSAVLNKGQFYELIKFRSKIRAGNRL 253
 138 -----KKDENGDKSVMTLLN--LH 155
 254 NCEVINWKEEN-----INWTLKNGEVLH 277

RESULT 5
 S38373
 Interleukin-1 beta precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
 C:Accession: S38373
 R:Van den Broeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
 Eur. J. Biochem. 217, 45-52, 1993
 A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic
 A:Reference number: S38373; MUID:94039070
 A:Accession: S38373
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <VAN>
 A:Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
 C:Genetics:
 A:Introns: 16/2; 33/3; 99/1; 154/1; 197/3
 C:Superfamily: interleukin-1

Query Match 10.0%; Score 80.5; DB 2; Length 267;
 Best Local Similarity 28.6%; Pred. No. 4.3; Mismatches 25; Indels 13; Gaps 6;
 Matches 24; Conservative 22;

53 DSEVRGLAVTLVKDSXSTLSCNK-----IISFEMDP--PENIDDIOSDLIFFOKRV 105
 165 DSDDK-IPVTLGIR-GKNLYLSCVMKNDPTLQLEDVDPKRYPKR--DMERFVFYKTEI 220
 106 PGHNKMEFESSLYEGHFLACQED 129

Db 221 --KNRYEFESALYPMYINSQAE 242

RESULT 6

D71461

hypothetical protein CT861 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: D71461

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, S.

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:99000809

A:Accession: D71461

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <ARN>

A:Cross-references: GB:AE001359; GB:AE001273; NID:g3329331; PIDN:AA66459.1; PID:g332933

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT861

Query Match 9.9%; Score 80; DB 2; Length 506;

Best Local Similarity 25.0%; Pred. No. 10;

Matches 38; Conservative 25; Mismatches 55; Indels 34; Gaps 7;

1 NGRLLCTAVININDOVLFDKRPVEFDMDDIOSASEPOTRLIYMYKSEVAGLA 60

63 SFSRLQPTTP-----KERILFFGS-SPSSQLSSVTRTTSSPNV-----LFSNSQTNST 111

61 VTLVSVDKSKSTLCKN-KIISFEEMDPENIDDIOSDLIFQKRVPGHNMKEFESSLY 118

112 RKISEKLFESSELSARSTKPSSEPIKPSSENL-----LHTPEHKK-ELFSSLK 159

119 EGHFLACQKEDDAF-----KLILKKRE 141

160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

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Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

Db 160 KDNLSPIMEIDFSFASFTESLEERLVQKKE 191

submitted to the EMBL Data Library, September 1995

A:Description: A 6.7 Kb fragment from chromosome VII of Saccharomyces cerevisiae cont

A:Reference number: S62051

A:Accession: S62055

A:Molecule type: DNA

A:Residues: 283-526 <COG>

A:Cross-references: EMBL:X91837; NID:g1177627; PIDN:CAA62954.1; PID:e203624; PID:g117

A:Experimental source: EMBL:Strain FY1679

R:Brusch, C.V.; Coglieva, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.

Submitted to the Protein Sequence Database, May 1996

A:Reference number: S64183

A:Accession: S64207

A:Molecule type: DNA

A:Residues: 1-526 <BRU>

A:Cross-references: EMBL:727212; NID:g1322810; PIDN:CAA696902.1; PID:e243794; PID:g132

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:CDG55

A:Cross-references: SGD:S0003158; MIPS:YGL190C

A:Map position: 7L

Query Match 9.8%; Score 79.5; DB 2; Length 526;

Best Local Similarity 25.0%; Pred. No. 12;

Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;

14 NINDOVL-FVDRKQPVFEDMTDIDOSASEPOTRLIYMYKSEVAGLAATLVSKDSKXST 72

213 DIPDQSFNIVDIKPTNKELEVTSAERHPQCNLFMYSSK-----GIKLCMDRONS 267

73 LSCNNKIISFEEMDPENIDDIOSDLIFQKRVPGHNMKEFESSLYEGHFLACQKEDDAF 132

268 L-CDNKTKEFEVLDLPINH-----FFTEITSSIDIKFSBN---GRVIAARD----- 311

133 KLILKKDENGKSVNFTLTNMQ 156

312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

Db 312 YLTVKIMDVNMDKPLKTI-NIHE 334

RESULT 8

E72734

hypothetical protein APE0413 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 17-Mar-2000

C:Accession: E72734

R:Kawabuchi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-uo, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339

A:Accession: E72734

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1039 <KAN>

A:Cross-references: DDBJ:AP000059; NID:95103911; PIDN:BA479369.1; PID:d1043155; PID:9

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0413

C:Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology

Query Match 9.7%; Score 78.5; DB 2; Length 1039;

Best Local Similarity 26.4%; Pred. No. 32;

Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;

31 DMTDIDOSASEPOTRLIYMY-----YKSEVAGLAATLVSKDSKXSTL 73

374 DIGRIDDELDEFEFLAIVDKLDDMFREELKKAQYVADIVGKAV-----DSKVETL 428

74 SCRNNKIISFEEMDPENIDDIOSDLIFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFK 133

429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 429 ---KILGLVLYPPPELPEFQDLA-SQKAIYFTEFKDVIATLYE-----K 471

Db 91 NATVVVYWNPIIPGVEV---GVGDTRVFSVLTINDLFCNTMIIGHDIYSCVPEFRNVN 146

OY 119 EGHFLACQKEDDAFKLLKKDKDNGKSVMTL 151

Db 147 YKRLTRIEDPFLNLRRLDDNNDFLLCFKL 179

RESULT 13

ICB01B

Interleukin-1 beta precursor - bovine

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999

C:Accession: J10010; S01380

R:Rajalszewska, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Moll, Immunol. 25, 429-437, 1988

A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin

A:Reference number: A94695; MUID:88318652

A:Accession: J10010

A:Molecule type: mRNA

A:Residues: 1-266 <MAL>

A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201

R:Leon, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.

Nucleic Acids Res. 16, 9054, 1988

A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A:Reference number: S01380; MUID:89016591

A:Accession: S01380

A:Molecule type: mRNA

A:Residues: 1-251, A', 253-266 <LEDO>

A:Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449

C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in

C:Comment: This protein lacks a conventional signal sequence for protein export. Cleaved

ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.

C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C:Superfamily: Interleukin-1

C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F:114-266/Product: Interleukin-1 beta #status predicted <MAL>

Query Match 9.5%; Score 77; DB 1; Length 266;

Best Local Similarity 26.0%; Pred. No. 8.9;

Matches 27; Conservative 24; Mismatches 33; Indels 20; Gaps 7;

OY 40 SEQOTRIIYMYKDESEVRG-----LAVTLVSDSKXSTLCKNK---LISFEEMP-- 87

Db 146 SQMNREVFVFCM--SFQGEERDNKIPVALGTD-KNLYLSCVAKGTPPLQLEVDPKV 202

OY 88 -PENIDDIQSLIFQKRVPGHNMKEFESSLYEGHFLACQKEDD 130

Db 203 YPKR--NMEKRVFYKTEI--KNTVERESVLYPMWISTQIEE 242

RESULT 14

T09378

hypothetical protein F23K16.250 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T09378

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16652.

A:Accession: T09378

A:Molecule type: DNA

A:Residues: 1-563 <BEV>

A:Cross-references: EMBL:AL078620; GSPDB:GNO0062; ATSP:F23K16.250

A:Experimental source: cultivar Columbia; BAC clone F23K16

C:Genetics:

A:Gene: ATSP:F23K16.250

A:Map position: 4

A:Introns: 118/3; 502/3

Query Match 9.5%; Score 77; DB 2; Length 563;

Best Local Similarity 23.6%; Pred. No. 21;

Matches 33; Conservative 29; Mismatches 40; Indels 38; Gaps 7;

OY 22 VDKRPQVFEDMDIDOSAS--EPOTRIIYMYKDESEVRGLATLSYKDS---KXSTLS- 74

Db 329 IDKAEVYFKMNDMNYIPSTFTECMIMMYGYGYSRAREIFEVEGESRVYKASTLA 388

OY 75 -----CKNKIISFEEMDPENIDDIQSLIFQKRVPGHNMKEF-----ESSLYEGHFLAC 125

Db 389 MLEVYCRNGLY-----LEADKLF-----HNSAFRVHPDASTYKFLYKAY 428

OY 126 OKED--DAFKLLKKDKDNG 143

Db 429 TKADMKEQVQILMKMKEXDG 448

RESULT 15

A64401

hypothetical protein M0809 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999

C:Accession: A64401

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodex,

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A:Reference number: A64300; MUID:96337999

A:Accession: A64401

A:Molecule type: DNA

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-167 <BUL>

A:Cross-references: GB:U67525; GB:L77117; NID:g1591497; PIDN:AAB98817.1; PID:g1499632

C:Genetics:

A:Map position: FOR733027-733530

Query Match 9.5%; Score 76.5; DB 2; Length 167;

Best Local Similarity 26.8%; Pred. No. 5.7;

Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

OY 47 IIVMYKDESEVRGLAVTLVYKDSK-----XSTLCKNKIISFEEMP--PENID 92

Db 38 IIVMYKDESEVRGLAVTLVYKDSK-----XSTLCKNKIISFEEMP--PENID 92

OY 93 DIQSLIFQKRVPGHNMKEFESSLYEGHFLACQKEDDAFKLLKKDKDNGKSVMTLT 152

Db 98 RLSSDDI-----LELNKKLDEG-----VKYIKLIFAELEH--KKVLLLEIK 136

OY 153 NLH 155

Db 137 DMH 139

Search completed: November 21, 2000, 23:19:59
job time: 6490 .sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 23:16:19 : Search time 32.92 Seconds
(without alignments)
152.364 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NEGRHCTTAVIRININDOVL.....KKDENGDKSVMTFLTNLHQS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues
Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806	99.8	192	1	IL18_MOUSE
2	736.5	91.2	194	1	IL18_RAT
3	538	66.6	193	1	IL18_HORSE
4	518	64.1	193	1	IL18_HUMAN
5	510	63.1	193	1	IL18_CANFA
6	509	63.0	192	1	IL18_PIG
7	82.5	10.2	803	1	LON_HAEN
8	82	10.1	267	1	IL1B_PIG
9	79.5	9.8	526	1	ZABA_YEAST
10	79	9.8	266	1	IL1B_BOVIN
11	78	9.7	1196	1	EXCN_CLOBO
12	77	9.5	885	1	UE3A_MOUSE
13	76.5	9.5	167	1	Y809_JENYA
14	76.5	9.5	621	1	HTPG_HELPY
15	76.5	9.5	706	1	YK70_YEAST
16	76	9.4	269	1	IL1B_MACMU
17	76	9.4	268	1	IL1B_MACNE
18	75.5	9.3	270	1	IL1A_MOUSE
19	75.5	9.3	439	1	Y811_JENYA
20	75.5	9.3	695	1	PRC_HAEN
21	75	9.3	265	1	IL1B_SHEEP
22	75	9.3	268	1	IL1B_MACFA
23	75	9.3	624	1	YBY3_SCHPO
24	74.5	9.2	270	1	IL1A_PIG
25	74	9.2	269	1	IL1B_HUMAN
26	74	9.2	1139	1	RBL2_HUMAN
27	73.5	9.1	589	1	TRPG_THEME
28	73	9.0	611	1	HBSL_YEAST
29	73	9.0	872	1	VP2_ROTTC
30	72.5	9.0	698	1	YB06_YEAST
31	72.5	9.0	1010	1	WNT5_DROME
32	72	8.9	207	1	ATPF_MYCPN
33	72	8.9	266	1	IL1B_CEREL

34	71.5	8.8	279	1	ATND_CAVPO
35	71.5	8.8	1215	1	ATG6_YEAST
36	71	8.8	165	1	HSCB_BUCAP
37	71	8.8	541	1	601M_HAEN
38	71	8.8	628	1	MSIN_HUMAN
39	71	8.8	1547	1	TOP2_BOMO
40	70.5	8.7	688	1	EFG_MYCPN
41	70.5	8.7	781	1	YB68_SCHPO
42	70	8.7	270	1	IL1A_FELCA
43	70	8.7	527	1	RAG2_MOUSE
44	70	8.7	747	1	AMD1_RAT
45	70	8.7	1381	1	YBE7_YEAST

ALIGNMENTS

RESULT 1
ID IL18_MOUSE STANDARD: PRT; 192 AA.
AC P70380:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER.
RX MEDLINE: 96061009.
RA Okamura H., Tsutsumi H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Toriige K., Okura T., Nukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.,
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=PANCREAS;
RX MEDLINE: 97174346.
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.,
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D49949; BAA08705.1; -;
DR EMBL: U66244; AAB49753.1; -;
DR MGD: MGI:107936; IL18.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLECT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA: 22135 MM: 8FED938473874D63 CRC64;
Query Match 99.8%; Score 806; DB 1; Length 192;

Best Local Similarity 99.4%; Pred. No. 7, 1e-67;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGLA 60
DB 36 NGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGLA 95
QY 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYEG 120
DB 96 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYEG 155
QY 121 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 157
DB 156 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 192

RESULT 2

IL18_RAT STANDARD: PRT: 194 AA.
AC P97636: P97637: 088749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY; TISSUE-ADRENAL GLAND;
RX MEDLINE: 97152963;
RA Conti B., Jahng J.W., Tanti C., Son J.H., Joh T.H.;
RT "Induction of Interferon-gamma inducing factor in the adrenal
cortex";
RT J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA";
RT Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC -----
CC EMBL: 077776; AAC53009.1;
DR EMBL: 077777; AAC53010.1;
DR EMBL: AJ22813; CA11001.1;
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA: 22303 MW: E2089AD6F1798450 CRC64;

Query Match 91.2%; Score 736.5; DB 1; Length 194;
Best Local Similarity 89.9%; Pred. No. 1, 6e-60;
Matches 142; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

QY 1 NGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGL 59
DB 37 NGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGL 96
QY 60 AVTLVSKDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 119
DB 97 AVTLVSKDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGHNMKEFESSLYE 156
QY 120 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 157
DB 157 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 194

RESULT 3

IL18_HORSE STANDARD: PRT: 193 AA.
AC 09XS07;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncaves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs";
RT Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
CC EMBL: Y11131; CAA72013.1;
DR EMBL: Y11131; CAA72013.1;
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA: 22058 MW: 4D81535E9004ECAF CRC64;

Query Match 66.6%; Score 538; DB 1; Length 193;
Best Local Similarity 68.8%; Pred. No. 2, 1e-42;
Matches 106; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

QY 2 FGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGLA 60
DB 38 FGRHCTTAATVIRININDOVLFDKRPVPEEDMTIDQASSEPOTRLIITYMKDSEVRGLA 97
QY 61 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 119
DB 98 VLTLSVDSKXSTLSCNKKIISFEEMDPENIDIOSDLIFFOKRVPGH-NKMEFESSLYE 157
QY 120 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 153
DB 158 HFLACOKEDDAFKLLKKDENGKSVMTFTLTNLHOS 191

RESULT 4
IL18_HUMAN STANDARD: PRT: 193 AA.
ID IL18_HUMAN

014116; 075599;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 96247646.
 RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
 RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
 RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 RT in Escherichia coli, and studies on the biologic activities of the
 RT protein.";
 RL J. Immunol. 156:4274-4279(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Linhua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA Corti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: D49950; BAA08706.1;
 DR EMBL: AF077611; AAC2787.1;
 DR EMBL: U90434; AAB50010.1;
 DR MIM: 600953;
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA: 22326 MW: 323C62C20378BD55 CRC64:

Query Match 64.1%; Score 518; DB 1; Length 193;
 Best Local Similarity 65.6%; Pred. No. 1.4e-40;
 Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGRHCTAVININDVLFVOK-RQPVFEDMTDIOASSEPTRLIIMYKDSVRGLA 60
 DB 38 FGRHCTAVININDVLFVOK-RQPVFEDMTDIOASSEPTRLIIMYKDSVRGLA 97
 QY 61 VLSVYKSKSTLSCNKKIISFEENDPENIDIOSDLFFQKRVPGH-NKKEFEESLYE 119
 DB 98 VLSVYKSKSTLSCNKKIISFEENDPENIDIOSDLFFQKRVPGH-NKKEFEESLYE 157
 QY 120 GHFLACQKEDDAFKILKKDKDENGKDSVMTFTLN 153
 DB 158 GHFLACQKEDDAFKILKKDKDENGKDSVMTFTLN 191

RESULT 5
 ID IL18_CANFA STANDARD: PRT: 193 AA.
 AC 09XSRO;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
 RT "Cloning, sequencing and characterization of canine interleukin-18.";
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y11133; CAA72015.1;
 DR EMBL: Y11133; CAA72015.1;
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 SO SEQUENCE 193 AA: 22037 MW: 0D973E586F461F25 CRC64:

Query Match 63.1%; Score 510; DB 1; Length 193;
 Best Local Similarity 64.9%; Pred. No. 7.4e-40;
 Matches 100; Conservative 25; Mismatches 27; Indels 2; Gaps 2;

QY 2 FGRHCTAVININDVLFVOK-RQPVFEDMTDIOASSEPTRLIIMYKDSVRGLA 60
 DB 38 FGRHCTAVININDVLFVOK-RQPVFEDMTDIOASSEPTRLIIMYKDSVRGLA 97
 QY 61 VLSVYKSKSTLSCNKKIISFEENDPENIDIOSDLFFQKRVPGH-NKKEFEESLYE 119
 DB 98 VLSVYKSKSTLSCNKKIISFEENDPENIDIOSDLFFQKRVPGH-NKKEFEESLYE 157
 QY 120 GHFLACQKEDDAFKILKKDKDENGKDSVMTFTLN 153
 DB 158 GHFLACQKEDDAFKILKKDKDENGKDSVMTFTLN 191
 RESULT 6
 ID IL18_PIG STANDARD: PRT: 192 AA.
 AC 019073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
 DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Muneta Y., Mori Y.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC
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 CC
 DR EMBL: U68701; AAC18415.1;
 DR EMBL: AB010003; BAA24135.1;
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 63.0%; Score 509; DB 1; Length 192;
 Best Local Similarity 64.9%; Pred. No. 9.1e-40;
 Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;

QY 2 FGRLHCTTAVIRINDVLYDK-RQPYFEDMTIDIOSASPPQRLIYMKDSEVGLA 60
 Db 37 FGKLEPLRSLIRINDVLYFVINOQHGVFEDMPDSDSNAPQTVFTIYMKDSLTLGLA 96
 QY 61 VLTLSVKRKKSTLSCKKRIISFEEMDPENDIOSPLDIFQKRVPGH-NKMEFESSLYE 119
 Db 97 VLTLSVQCKKSTLSCKKRIISFEEMDPENDIOSPLDIFQKRVPGH-NKMEFESSLYE 156
 QY 120 GHFLAQCKEDDAFKLLIKKDKDNGSKSVMTLTN 153
 Db 157 GYFLACKKENDLFLKLLKEKDECGDKSIMFTVON 180

RESULT 7
 LON_HAEIN STANDARD; PRT; 803 AA.
 AC P43864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ATP-DEPENDENT PROTEASE LA (EC 3.4.21.35).
 GN LON OR LON-A OR H10462.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-RD / KW20;
 RX MEDLINE: 95350630.
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gehrm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd."
 RL Science 269:496-512(1995).

CC -1- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
 CC IN PRESENCE OF ATP. DEGRADATES THE REGULATORY PROTEINS RC3A AND
 CC SUIA. HYDROLYSES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
 CC PROTEIN SUBSTRATE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
 CC CASEIN AND DENATURATED SERUM ALBUMIN, IN PRESENCE OF ATP.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
 CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
 CC
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 CC
 DR EMBL: U32729; AAC22121.1;
 DR TIGR: H10462;
 DR INTERPRO: IPR001939;
 DR INTERPRO: IPR001984;
 DR PFAM: PF00004; AAA; 1.
 DR PRINTS: PR00830; ENDOLAPYASE.
 DR PROSITE: PS01046; LON_SER; 1.
 KW Hydrolase; Serine protease; ATP-binding.
 FT NP_BIND 356 363 ATP (POTENTIAL).
 FT ACT_SITE 679 679 BY SIMILARITY.
 SQ SEQUENCE 803 AA; 89347 MW; 9E590852611EEA5B CRC64;

Query Match 10.2%; Score 82.5; DB 1; Length 803;
 Best Local Similarity 18.9%; Pred. No. 4.3; 71; Indels 85; Gaps 7;
 Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

QY 3 GRHLCTTAVIRINDVLYDKR-----QPYFEDMTIDIOSAS----- 40
 Db 30 GRKSLNALLEANADKOLLVSGREADLEPTPEDLPDGTIANIOLKLPDITVKYL 89
 QY 41 -EPQTRLIYMKDSE-----VGLAVTLVSKDSKXSLTSCNKKIISFE 83
 Db 90. VEGONAKIINSLDGEKCFSAQITPIETTYGDEKELVAKSAVASENYLTNKKRVPD 149
 QY 84 EMPDPENIDDI-----OSDLFFQK 103
 Db 150 ILNALQRIDVDRLADTMAAHLFVIRHKONALELANVOERLEYLLGMASEADIIQVER 209
 QY 104 RVPGNKMEFESSLYEGHFLAQCKEDDAFKLLIKKDKDNGSKSVMTLTNMQ 156
 Db 210 RINGRVKQWKEK-GRNYVL-----NEQIKAIRKEMDGENEDTIDEVEQLHQ 256

RESULT 8
 IL1B_PIG STANDARD; PRT; 267 AA.
 AC P26889;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93314975.
 RA Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
 RT "Cloning, sequencing and regulation of an mRNA encoding porcine
 RT interleukin-1 beta."
 RL Gene 129:285-289(1993).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC
 CC -1 SUBUNIT: MONOMER.
 CC
 CC -1 DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC
 CC -1 MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC
 CC -1 SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC
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 CC
 CC
 CC EMBL, M86725; AA02584.1; -
 CC PIR, JN0724; JN0724.
 CC HSSP, P01584; 1H1B.
 CC INTERPRO: IPR000975; -
 CC INTERPRO: IPR002348; -
 CC PFMAM, PF00340; Interleukin-1; 1.
 CC PRINTS: PR00262; IL1HBF.
 CC PRINTS: PR00264; INTERLEUKIN_1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 CC PROPEP 1 114 BY SIMILARITY
 CC CHAIN 115 267 INTERLEUKIN-1 BETA.
 CC SEQUENCE 267 AA; 30404 MW; 7EB92B784D5086F CRC64;
 SQ
 Query Match 10.1%; Score 82; DB 1; Length 267;
 Best Local Similarity 26.1%; Pred. No. 1.3; Indels 12; Gaps 5;
 Matches 23; Conservative 22; Mismatches 31;
 QY 49 YWKDSEVGLAVLTSLVSKXSTLSCNKK---IISFEMDP--PENIDIQSDLIFF 101
 DB 160 FVQGDSDNNKIKPTVLTGK-GKNLYLSCVAKDWTPTLQLEDIDPKRYPKR--DMERFVRY 216
 QY 102 QKRVPGHNKMEFESSLYEGHFLACQKED 129
 DB 217 KTEI--KNRVEFESALYPMWYSTSOAE 242
 RESULT 9
 2ABA_YEAST STANDARD: PRT: 526 AA.
 ID 2ABA_YEAST
 AC 000362;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1989 (Rel. 38, Last annotation update)
 DE PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT B (PR55) (CELL DIVISION
 DE CONTROL PROTEIN 55).
 GN CDC55 OR YGL190C OR G1345.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92017858.
 RA Healy A.M., Zolnierowicz S., Stapleton A.E., Goebel M.,
 RA Depooll-Roach A.A., Pringle J.R.,
 RT "CDC55, a Saccharomyces cerevisiae gene involved in cellular
 RT morphogenesis: identification, characterization, and homology to the
 RT B subunit of mammalian type 2A protein phosphatase.",
 RL Mol. Cell. Biol. 11:5767-5780(1991).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / FY1679;
 RX MEDLINE: 97167971.
 RA Cogollevia M., Klima R., Bertani I., Delneri D., Zaccaria P.,
 RA Brusch C.V.;
 RT "Sequencing of a 40.5 kb fragment located on the left arm of
 RT chromosome VII from Saccharomyces cerevisiae".
 RT Yeast 13:55-64(1997).
 CC
 CC -1 FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
 CC IN THE CELL, SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
 CC CELLULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
 CC CRITICAL SUBSTRATES FOR THIS PHOSPHATASE. THE REGULATORY SUBUNIT
 CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT OVERLAPPING,
 CC SUBSETS OF SUBSTRATES.
 CC
 CC -1 SUBUNIT: PP2A EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH
 CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
 CC A 65 KDA (PR55) (SUBUNIT A) AND A 55 KDA (PR55) (SUBUNIT B)
 CC REGULATORY SUBUNIT.
 CC
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
 CC FAMILY.
 CC
 CC -----
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 CC
 CC
 CC EMBL, M72716; AA34482.1; -
 CC EMBL, Z72712; CA96902.1; -
 CC EMBL, X91837; CA62954.1; -
 CC EMBL, X91489; CA62785.1; -
 CC PIR, A1698; A41698
 CC SGD, S0003158; CDC35.
 CC INTERPRO: IPR000009; -
 CC PFMAM, PF01240; PR55; 1.
 CC PRINTS: PR00600; PP2APR55.
 CC PROSITE: PS01024; PR55_1; 1.
 CC PROSITE: PS01025; PR55_2; 1.
 CC Cell cycle.
 CC
 CC
 CC DOMAIN: 416 419 POLY-SER.
 CC CONFLICT 500 500 I->N (IN REF. 1).
 CC SEQUENCE 526 AA; 59662 MW; 6DA12C2805FA6A82 CRC64;
 SQ
 Query Match 9.8%; Score 79.5; DB 1; Length 526;
 Best Local Similarity 23.0%; Pred. No. 4.9;
 Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;
 QY 14 NINDOVL-FVDRKQVPEMDPIDQASASEPQRLTIYWKDSEVGLAVLTSLVSKXST 72
 DB 213 DIPDOSFNIVDKPTNMEELTIVTSAEFHPOECLPMYSSK-----GTILCDMRONS 267
 QY 73 LSCNKKIISFEMDPENIDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDAF 132
 DB 268 L-CDNKRTTFEEDYLDPIHNH-----FFETITSSIDIKFSPN---GRYIASRD----- 311
 QY 133 KILKKKDEGDKSVFILTILNHO 156
 DB 312 YLTVKIMVNMMDKPKLKIT-NIHE 334
 RESULT 10
 IL1B_BOVIN STANDARD: PRT: 266 AA.
 ID IL1B_BOVIN
 AC P09428;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 RN IL1B
 OS Bos taurus (Bovine).

RT "Subcellular localization and ubiquitin-conjugating enzyme (E2)
 RT interactions of mammalian HECT family ubiquitin protein ligases."
 RL J. Biol. Chem. 272:15085-15092(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX SUTCLIFFE J.S., JIANG Y.-H., GALJAARD R.-J., MATSUURA T., FANG P.,
 RA KUBOTA T., CHRISTIAN S.L., BRESSLER J., CATTANACH B., LEDBETTER D.H.,
 RA BEAUDAT A.L.;
 RT "The E6-AP ubiquitin-protein ligase (UBE3A) gene is localized within
 RT a narrow Angelman syndrome critical region."
 RL Genome Res. 7:368-377(1997).
 CC -1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM
 CC AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND
 CC THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.
 CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
 CC THIOESTER FORMATION.
 CC -1- SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
 CC DOMAIN.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL: U96636; AAB63361.1; -
 DR EMBL: U82122; AAB47756.1; -
 DR MGD: MGI105096; UBE3A.
 DR INTERPRO: IPR000569; -
 DR INTERPRO: IPR002106; -
 DR PFM: PFM0632; HECT. 1.
 DR PROSITE: PS50237; HECT. 1.
 DR KW Nuclear protein; Ubiquitin conjugation; Ligase.
 FT DOMAIN 405 410
 FT BINDING 786 885
 FT BINDING 853 853 UBIQUITIN (BY SIMILARITY).
 FT CONFLICT 187 187 D -> E (IN REF. 2).
 FT CONFLICT 301 301 L -> V (IN REF. 2).
 FT CONFLICT 343 343 T -> S (IN REF. 2).
 FT CONFLICT 384 384 N -> K (IN REF. 2).
 FT CONFLICT 460 460 S -> F (IN REF. 2).
 FT CONFLICT 486 486 G -> F (IN REF. 2).
 FT CONFLICT 535 535 T -> R (IN REF. 2).
 FT CONFLICT 577 582 DEGVG -> MREAF (IN REF. 2).
 FT CONFLICT 584 584 E -> S (IN REF. 2).
 FT CONFLICT 587 588 QL -> SW (IN REF. 2).
 FT CONFLICT 597 597 D -> N (IN REF. 2).
 FT CONFLICT 623 627 FTLLG -> VYSDWH (IN REF. 2).
 FT CONFLICT 725 726 IS -> NL (IN REF. 2).
 FT CONFLICT 817 817 L -> O (IN REF. 2).
 FT CONFLICT 869 870 NV -> KE (IN REF. 2).
 FT SEQUENCE 885 AA; 101175 MW; 550885E080CCB699 CRC64;

Query Match 9.5%; Score 77; DB 1; Length 885;
 Best Local Similarity 26.7%; Pred. No. 15;
 Matches 31; Conservative 20; Mismatches 35; Indels 30; Gaps 7;

OY 14 NINDOVLVDRKQPVF--DWTIDIDQASSEPOTRLIYMYKDSVRLAVLTVKSDSKXS 71
 DB 402 NHNEE-----DDEEPIPESSSELTQLGELDERRNK-----KGRVDPLETLGVK----- 446
 OY 72 TLSCNNKIISSEEM--DPENIDIOQLIFQKRVPGHNNKMEFESSLYEGHFLAC 125
 DB 447 TLDCKRLPISSEESINELNVLNLEMDKYTF-----KVTEN--KQSFMTG 491

RESULT 13
 ID Y809.METJA STANDARD; PRT; 167 AA.
 AC 058219;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE HYPOTHETICAL PROTEIN MJ0809.
 GN MJ0809.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 CC Methanococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE: 96337999.
 RA BALT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
 RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
 RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
 RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
 RA SCOTT J.L., GEORGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
 RA UTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
 RA COLTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
 RA KLEIN H.-P., FRASER C.M., SMITH H.O., WOESSE C.R., VENTER J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: BELONGS TO THE M.JANNASCHII MJ0553 / MJ0809 / MJ1331 /
 CC MJ1405 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U67525; AAB98817.1; -
 DR TRIGR: MJ0809; -
 DR KW Hypothetical protein.
 FT SEQUENCE 167 AA; 19723 MW; DD998FE1329C0042 CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 167;
 Best Local Similarity 26.8%; Pred. No. 2.3;
 Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

OY 47 IIVYKDSVRLAVLTVKDSK-----XSTLSCNNKIISFEEMDP-----PENID 92
 DB 38 IIVYKDSVRLAVLTVKDSK-----XSTLSCNNKIISFEEMDP-----PENID 92
 OY 93 DIOSDLIFQKRVPGHNNKMEFESSLYEGHFLACOKEDDAFLIKKDENGKSVMTLT 152
 DB 98 RLSSDDI-----LELNKKLDEG-----VKYIKLIFAELEEH--KKVLLEIK 136
 OY 153 NLH 155
 DB 137 DMH 139
 RESULT 14
 ID HTPG_HELPY STANDARD; PRT; 621 AA.
 AC P56116;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
 GN HTPG OR HP0210.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

```
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-26695 / ATCC 700392;
RX MEDLINE: 97394467.
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Letten B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
CC -----
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DR EMBL: AE000541; AAD07278.1; -
DR HSSP: P07900; IYES.
DR TIGR: HP0210; -
DR INTERPRO: IPR001404; -
DR PFAM: PFO0183; HSP90; 1.
DR PRINTS: PR00775; HEATSHOCK90.
DR PROSITE: PS00298; HSP90; 1.
DR Chaperone: ATP-binding; Heat shock.
KW SEQUENCE 621 AA; 71274 MW; 28F198C1DC7EAB9A CRC64;
SQ
```

Query Match
Best Local Similarity 23.2%; Score 76.5; DB 1; Length 621;
Matches 29; Conservative 27; Mismatches 52; Indels 17; Gaps 4;

```
OY 32 MTDIDQASEPQRLIIYMYKDSVGRGLAVTLISVKK--DSKXSTLSCKNKLISFEEDMP 88
DB 31 LRELVSANSPALDKLWMLTDEKLGINTPISHLSPDSQKTLIKNGIGMDNDLI 90
OY 89 ENIDDI-QSDLIFFQKRVPGHNK-----EFSSLYEGHFLACQKEDDAFKLLKKDE 141
DB 91 EHLGITAKSGTKNLFSLALSGDKKKDSALIGQFGVGYSAFMVAS-----KIVQITKKV 143
OY 142 NGDKS 146
DB 144 NSDOA 148
```

RESULT 15
YK70 YEAST
ID YK70 YEAST STANDARD: PRT; 706 AA.
AC P36166;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HYPOTHETICAL 79.4 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.
GN YKR090W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Baladron V., Ballester J.P.G., Bou G., del Rey F., Esteban P.F.,
RA Garcia-Cantalejo J.M., Garcia-Ramirez J.J., Gonzalez A., Jimenez A.,

```
RA Revuelta J.L., Santos M.A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
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```

```
DR EMBL: Z28315; CA882169.1; -
DR PIR: S38168; S38168.
DR SGD: S0001798; YKR090W.
DR INTERPRO: IPR001781; -
DR PFAM: PFO0412; LIM; 2.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS00293; LIM_DOMAIN_2; 2.
KW Hypothetical protein; LIM motif; Metal-binding; Zinc.
FT DOMAIN 556 612
FT DOMAIN 621 672
FT LIM.
SQ SEQUENCE 706 AA; 79447 MW; B27DB9E09A39AA42 CRC64;
```

Query Match
Best Local Similarity 22.2%; Score 76.5; DB 1; Length 706;
Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;

```
OY 9 TAVININDQVLFVDKROVFEDMTDIDQASEPQ-----RLIYMYKDSVGRGLAVTLIS 64
DB 428 TSIYONSNTNL-----SROTILVDKGVDEDAPESTNGGPIFYFKQSNVE-----YS 478
OY 65 VKDSKXSTLSCKNKLISFE--EMDPENIDDIQSDLIFFQKRVPGH----- 108
DB 479 NNEGMSQSETFRTKPLTEALQLQHKRNITDLREE--INSNKSNSHVLPNGGTRYSSDA 537
OY 109 -----NKMFEFSSLYEGHFLACQKEDDAFKLLKKDE 141
DB 538 DYKETPELFKYPGEGPCACGLGVTKRMFSKENE 575
```

Search completed: November 21, 2000, 23:21:41.
Job time: 322 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 2000, 21:56:14 Search time 46.58 seconds
(without alignments)
314.722 Million cell updates/sec

Title: US-09-050-249-2

Perfect score: 808
Sequence: 1 NEGRHCTTAVIRINDOVL.....KKDENGDKSVMTLTNHS 157

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_14:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522	64.6	193	09UT73	09UT73 bos taurus
2	91	11.3	987	09V718	09V718 drosophila
3	85.5	10.6	784	09Y174	09Y174 schistosoma
4	85.5	10.6	784	09Y9R6	09Y9R6 schistosoma
5	85	10.5	482	09U0A4	09U0A4 dictyosteli
6	83	10.3	483	09Y0A6	09Y0A6 dictyosteli
7	83	10.3	267	073909	073909 gallus galli
8	81	10.0	483	09XV67	09XV67 caenorhabdi
9	80.5	10.0	267	029082	029082 sus scrofa
10	80.5	10.0	414	024892	024892 elmeria max
11	80	9.9	506	084869	084869 chlamydia t
12	78.5	9.7	1039	09YF27	09YF27 aeropyrum p
13	78	9.7	388	09RF7	09RF7 streptococc
14	78	9.7	1196	045916	045916 clostridium
15	78	9.7	1196	053550	053550 clostridium
16	78	9.7	1196	038197	038197 clostridium
17	78	9.7	1196	092X77	092X77 clostridium
18	78	9.7	1247	096168	096168 plasmodium
19	77.5	9.6	366	09YMM0	09YMM0 lymantria d

20	77.5	9.6	1631	4	09Y6U6	09Y6U6 homo sapien
21	77	9.5	563	10	09SV96	09SV96 arabidopsis
22	77	9.5	672	5	09U0K1	09U0K1 plasmodium
23	76.5	9.5	905	3	094641	094641 schistosach
24	76.5	9.5	1294	10	09S814	09S814 arabidopsis
25	76	9.4	525	4	09UF58	09UF58 homo sapien
26	75.5	9.3	161	11	062161	062161 mus musculu
27	75.5	9.3	626	2	050498	050498 streptomyce
28	75.5	9.3	818	10	09SHN7	09SHN7 arabidopsis
29	75.5	9.3	866	10	024295	024295 pisum sativ
30	75	9.3	621	2	09ZM2	09ZM2 heliobacte
31	75	9.3	1146	2	051778	051778 borrelia bu
32	74.5	9.2	661	2	P73025	P73025 synechocyst
33	74.5	9.2	803	4	075283	075283 homo sapien
34	74.5	9.2	849	11	09Z283	09Z283 mus spretus
35	74.5	9.2	950	4	09UN73	09UN73 homo sapien
36	74	9.2	254	2	051029	051029 borrelia bu
37	74	9.2	445	5	09XVW4	09XVW4 drosophila
38	73.5	9.1	647	3	002892	002892 saccharomyc
39	73.5	9.1	680	3	074343	074343 schizosacch
40	73.5	9.1	1128	10	09SAF6	09SAF6 arabidopsis
41	73.5	9.1	1146	2	068317	068317 vibrio chol
42	73.5	9.1	2077	12	09WT33	09WT33 human herpe
43	73.5	9.1	2077	12	09Q037	09Q037 human herpe
44	73	9.0	266	6	09TRK1	09TRK1 tursiops tr
45	73	9.0	1298	5	044199	044199 caenorhabdi

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	193 AA
ID	09UT73			
AC	09UT73			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	INTERLEUKIN-18 PRECURSOR.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 20012648.			
RA	Shoda L.R., Zarling D.S., Hirano A., Brown W.C.;			
RT	"Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-			
RT	18 expression in macrophages and its IFN-gamma-inducing activity.";			
RL	J. Interferon Cytokine Res. 19:1169-1177(1999).			
DR	EMBL: AF124789; AAF08686.1; -			
DR	SEQUENCE. 193 AA; 22347 MW; 65720F199DENA9C4 CRC64;			

Query Match 64.6%; Score 522; DB 6; Length 193;
Best Local Similarity 65.2%; Pred. No. 1.2e-40;
Matches 101; Conservative 30; Mismatches 22; Indels 2; Gaps 2;

QY	1	NEGRHCTTAVIRINDOVLVDK-ROPVFEDMTDIDQASSEPOTRLITYRKSEVAGL	59
DB	1	NEGRHCTTAVIRINDOVLVDK-ROPVFEDMTDIDQASSEPOTRLITYRKSEVAGL	59
QY	37	HFGLEKRLSIIRNLVINGNOVPFEDMPSDCSDNAPOTIFIIYWKSLTGL	96
DB	37	HFGLEKRLSIIRNLVINGNOVPFEDMPSDCSDNAPOTIFIIYWKSLTGL	96
QY	60	AVTISVDSKSTLSCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	118
DB	60	AVTISVDSKSTLSCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	118
QY	97	AVTISVDSKSTLSCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	156
DB	97	AVTISVDSKSTLSCKNKIISFEEMDPENIDIOSDLFFOKRVGH-NKMEFESSLY	156
QY	119	EGHFLACOKEDDAFLIKKKDENGDKSVMTLTN	153
DB	119	EGHFLACOKEDDAFLIKKKDENGDKSVMTLTN	153
QY	157	KGYFLACKENDFLIKKKDENGDKSVMTLTN	191
DB	157	KGYFLACKENDFLIKKKDENGDKSVMTLTN	191
RESULT	2		
QYV718			


```

ID 09Y718 PRELIMINARY: PRT: 987 AA.
AC 09Y718:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG8414 PROTEIN.
GN CG8414.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY.
RX MEDLINE: 20196006.
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherf S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Plannoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fioder C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merilov G., Mishina N.V., Mobarry C., Morris J., Mosnere A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003808; AAF58067.1;
DR FLYBASE: FBgn0034073; CG8414.
SQ SEQUENCE 987 AA: 110425 MW: E10CD3B7810BCAA CRC64:

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Query Match 11.3%; Score 91; DB 5; Length 987;
Best Local Similarity 31.5%; Pred. No. 2.7;
Matches 35; Conservative 21; Mismatches 47; Indels 8; Gaps 5;
OY 24 KROP-FEEDMTDIDQASSEPOTRLITYMKDSVGRGLATVLSKDSKXSLCKNNIISF 82
DB 373 QREPLIEELFD-DPEVEKQERIEQSVMDIYVKNLSSVPPKRESEVAITEENDEVS 431
OY 83 EEMDPENIDIDIO-SDLIFOKRVGNHMKME--FESSYEGHFLCOKED 129
DB 432 PEVVTPEKEVYLOPSPVPPY--RNQANPTELSEVENSLSNNVLAIVNED 480

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RESULT 3
09Y1J4

```

ID 09Y1J4 PRELIMINARY: PRT: 784 AA.
AC 09Y1J4:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RETINOID X RECEPTOR RXR-2.
GN RETINOID X RECEPTOR RXR-2.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NMRI.
RX MEDLINE: 99307140.
RA Freebern W.J., Niles E.G., Lloverde P.T.:
RT "RXR-2, a member of the retinoid x receptor family in Schistosoma
RL mansoni."
RL Gene 233:33-38(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF129816; AAD33428.1;
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000336;
DR INTERPRO: IPR001628;
DR PFAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
SQ SEQUENCE 784 AA: 87249 MW: C035E449E5F547F CRC64:

```

```

Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;
OY 46 LIYMKSEVGLAVITVSKSKSTLCKNKIISFEEMPPEN-IDDIOSDLIF----- 100
DB 513 LVYWLANDKPRSLSTSTSKLPPTTINSTDISNTDPPENSISDISKDTIOKK 572
OY 101 FOKRVGNHMKME-FESSYEGHFLCOKEDDAFKLILKKDENGDSVMTNLHQS 157
DB 573 IKSVPLDEKMDYVSNRPEFLL-----NNLTFRPHNNNDSSSKPTINDM 621
RESULT 4
ID 09Y9R6 PRELIMINARY: PRT: 784 AA.
AC 09Y9R6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RETINOID X RECEPTOR.
GN RETINOID X RECEPTOR.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NMRI.
RX MEDLINE: 99307140.
RA Mendonca R.L., Escrivá H., Bouton D., Vanacker J.-M., Zelus D.,
RA Bonnelly E., Pierce V.:
RT "A Schistosoma mansoni nuclear receptor of the RXR family shows marked
RT structural and functional divergence from vertebrate and arthropod
RT homologs."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF158102; AAD45325.1;
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000536;
DR INTERPRO: IPR001628;
DR INTERPRO: IPR001723;
DR PFAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDINGER.

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DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMONER.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor
SO SEQUENCE 784 AA; 87250 MW; 471DAE69EB135A9F CRC64;

Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;

QY 46 LIYWKDSEVGLAVLTVKDKSKXSTLCKNKKISFEEMDPEN-IDDIOSDLIF---- 100
D 513 LVYWLANDHKKRSLSTNSSTSKLPTPTINSTDISNITDDEPNISDISKDTIQMKK 572
OY 101 FOKRPGHNKE-FESSLYEGHFLACQKEDDAFKLLKKKDKNGSKSVFTITNHOS 157
D 573 INKSVPLDEKMDYYNSPEPHLL-----NNLTKPMNNNDSSISKPTNINDN 621

RESULT 5

Q9UA14 PRELIMINARY; PRT; 482 AA.

AC Q9UA14:
DT 01-MAY-2000 (Tremblrel. 13; Created)
DT 01-MAY-2000 (Tremblrel. 13; Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14; Last annotation update)
DE PROTEIN PHOSPHATASE 2A 55 KDA REGULATOR B SUBUNIT (FRAGMENT).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99379588.
RA Murphy M.B., Levi S.K., Egelhoff T.T.;
RT "Molecular characterization and immunolocalization of Dictyostelium
RL FEBS Lett. 456:7-12(1999).
DR EMBL; AF138279; AAD2694.1; -
DR INTERPRO; IPR000009; -
DR INTERPRO; IPR001680; -
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; P2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
FT NO_TERM 1
SQ SEQUENCE 482 AA; 55107 MW; 95E879E7A37D2392 CRC64;

Query Match 10.5%; Score 85; DB 5; Length 482;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;

QY 14 NINDOVL-FVKKRQPFEDMTDIDQASAPOTRLIYWKDSEVGLAVLTVKDKSKXST 72
D 236 NINTECFNVVDIKPTNMDLLEVTISAEFHTSCIFPMYSSK-----GTIKGLDRSSA 290
OY 73 LSCNKKIISFEEMDPENIDDIOSDLIFOKRVPGHNKEFESSLYEGHFLACQKEDDAF 132
D 291 L-CDNHAAVFEYEDPSNKS-----FFSELISSISDIKFSR---DGRYILSRD----- 334
OY 133 KLILKKDKNGSKSVFTL 151
D 335 FLTKLMDINMKNPKVKTI 353

RESULT 6
Q9Y0A6 PRELIMINARY; PRT; 483 AA.

AC Q9Y0A6:
DT 01-NOV-1999 (Tremblrel. 12; Created)
DT 01-NOV-1999 (Tremblrel. 12; Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13; Last annotation update)

DE PROTEIN PHOSPHATASE 2A B55 REGULATORY SUBUNIT.
GN pppd.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX4;
RA Campanha R.B., Etcheberry L.C., da Silva A.M.;
RT "Functional analysis of a B regulatory subunit of protein phosphatase
RT 2A in D. discoideum"; to the EMBL/GenBank/DBJ databases.
RL EMBL; AF167979; AAD45396.1; -
DR INTERPRO; IPR000009; -
DR INTERPRO; IPR001680; -
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; P2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
SQ SEQUENCE 483 AA; 55375 MW; DCF9434FE95C27BE CRC64;

Query Match 10.5%; Score 85; DB 5; Length 483;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;

QY 14 NINDOVL-FVKKRQPFEDMTDIDQASAPOTRLIYWKDSEVGLAVLTVKDKSKXST 72
D 237 NINTECFNVVDIKPTNMDLLEVTISAEFHTSCIFPMYSSK-----GTIKGLDRSSA 291
OY 73 LSCNKKIISFEEMDPENIDDIOSDLIFOKRVPGHNKEFESSLYEGHFLACQKEDDAF 132
D 292 L-CDNHAAVFEYEDPSNKS-----FFSELISSISDIKFSR---DGRYILSRD----- 335
OY 133 KLILKKDKNGSKSVFTL 151
D 336 FLTKLMDINMKNPKVKTI 354

RESULT 7

ID 073909 PRELIMINARY; PRT; 267 AA.

AC 073909:
DT 01-AUG-1998 (Tremblrel. 07; Created)
DT 01-AUG-1998 (Tremblrel. 07; Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13; Last annotation update)
DE INTERLEUKIN-1BETA.
GN IL-1BETA.
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA Weinig K.C., Sick C., Kaspers B., Staeheli P.;
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15006; CA475239.1; -
DR HSSP; P18510; IIRA.
DR INTERPRO; IPR000975; -
DR PFAM; PF00340; Interleukin-1; 1.
DR PROSITE; PS00253; INTERLEUKIN-1; 1.
FT CHAIN 106 267 INTERLEUKIN-1BETA.
SQ SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;

Query Match 10.3%; Score 83; DB 13; Length 267;
Best Local Similarity 24.8%; Pred. No. 3.2;
Matches 30; Conservative 18; Mismatches 45; Indels 28; Gaps 4;

QY 31 DMTDIDQ-----ASEPOTRLIYWKDSEVGLA-----VTLTVK 66
D 118 DIFDINQCFVLESPTQVALVHLQGPSSSQKVRNLIALYRBRPGSGAGTQMPVALGIK 177

	Q29082..	PRELIMINARY;	PRT;	267 AA.
AC	Q29082..			
DT	01-NOV-1996 (TEMBLrel..01, Created)			
DT	01-NOV-1996 (TEMBLrel..01, Last sequence update)			
DT	01-MAY-2000 (TEMBLrel..13, Last annotation update)			
DE	INTERLEUKIN 1-BETA.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER.			
RA	Vanderbroeck K.;			
RL	Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE: 94039070.			
RA	Vanderbroeck K., Fiten P., Beuken E., Martens E., Janssen A.,			
RT	Van Damme T., Opdenakker G., Billiau A.;			
RT	"Gene sequence, cDNA construction, expression in <i>Escherichia coli</i> and			
RT	genetically approached purification of porcine interleukin-1 beta."			
RL	Eur. J. Biochem. 217:45-52(1993).			
DR	EMBL: X74566; CA52660.1; ..			
DR	HSSP: P01584; 1H1B.			
DR	INTERPRO: IPR002975; ..			
DR	INTERPRO: IPR002348; ..			
DR	PFAM: PF00340; interleukin-1; 1.			
DR	PRINTS: PR00262; I1IHGF.			
DR	PRINTS: PR00264; INTERLEUKIN1.			
DR	PROSITE: PS00253; INTERLEUKIN1..1			
QO	SEQUENCE 267 AA; 28993 MW; 4830645DA5FF9667 CRC64;			

	Query Match:	10.0%;	Score	80.5;	DB	6;	Length	267;
	Best Local Similarity	28.6%;	Pred.	No.	5.5;			
	Matches	24;	Conservative	22;	Mismatches	25;	Indels	13;
	Gaps							6
QY	53 DSEVRGLAVTLVKDCKKXSTLSCNRK----	IISFEEMP--PENIDDIOSDLFFPOKR	V	105				
Db	165 DSDDK-IPVTLGIK-GKNLYLSGVAKKDPTPLQLDEDVDPKSYPRR--DMEKRFVFYKTEI	220						
QY	106 PGHNKMEFESSLYEGHFLAACOKED	129						
Db	221 --KNRYEFESALYPWNYISTSQAE	242						
RESULT	10							
Q24892								
ID	Q24892	PRELIMINARY;	PRT:	414 AA.				
AC	Q24892;							
DT	01-NOV-1996 (Tremblrel. 01, Created)							
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)							
DT	01-JUN-2000 (Tremblrel. 14, Last annotation update)							
DE	CALMODULIN-DOMAIN PROTEIN KINASE (FRAGMENT).							
OS	Eimeria maxima.							
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;							
CC	[1].							
RN	SEQUENCE FROM N.A.							
RP	STRAIN-HOUGHTON;							
RC	MEDLINE; 96089387.							
RX	Bumstead J.M., Dunn P.P.J., Tomley F.M.;							
RA	"Nitrocellulose immunoblotting for identification and molecular gene							
RT	cloning of Eimeria maxima antigens that stimulate lymphocyte							
RL	proliferation."							
RT	clin. Diagn. Lab. Immunol. 2:524-530(1995).							
RN	[2]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN-HOUGHTON;							
RP	MEDLINE; 97048698.							
RX	Dunn P.P.J., Bumstead J.M., Tomley F.M.;							
RT	"Sequence, expression and localization of calmodulin-domain protein							

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Query Match Similarity      9.9% Score 80; DB 2; Length 506;
Best Local Similarity      25.0% Pred No. 13;
Matches      38; Conservative      25; Mismatches      55; Indels      34; Gaps      7

Oy      1 NGRHLCTTAIVIRNINDOVLFDVKROPFEDMTDIDOSASEPOTRLIIYKDESEVGLA 60
      :|||      :|||      :|||      :|||      :|||      :|||
Db      63 SFSRIQPTTP-----KERILFFGS-SPSSQLSTVTRITTTSSPNW-----LFSNSQTRNST 111

Oy      61 VFLSVKDSKXSLTSCKN--KIISFEEMDPENPIDIOSDLIFQKRVPGHKNKEFESSLY 118
      |||      |||      |||      |||      |||      |||
Db      112 RKLSEKLHSESLSANDSTKRPSSSEPIKRSENL-----LHTPEHKK-ELSSSLK 159

Oy      119 EGHFLACOKEDDAF-----KLLKKKDE 141
      :|||      :|||      :|||      :|||      :|||
Db      160 KDLSPIMEIIDSFSAEITESLEERLYTKREE 191

RESULT      12

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RESULT 13
O9RF17
ID O9RF17 PRELIMINARY; PRT: 388 AA.
AC O9RF17;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PROTEIN I/II V-REGION (FRAGMENT).
OS Streptococcus gordonii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P4A1.
RA Chatenay-Rivarday C., Yamodo I., Sciotti M.A., Troffer-Charlier N.,
RA Kleijn J.P., Ogier J.;
RA "Tribalpa release by monocytic THP-1 cells through cross-linking of
RI the extended V-region of the oral streptococcal protein I/II.";
RI J. Leucoc. Biol. 0:0-0(2000).
RL EMBL: AF192472; AAF20187.1; -.
DR
DR NON_TER 1
FT 388 388

```

SQ SEQUENCE 388 AA: 42720 MW: 907F6A76805BCE45 CRC64;
 Query Match 9.7%; Score 78; DB 2; Length 388;
 Best Local Similarity 20.1%; Pred. No. 14;
 Matches 27; Conservative 25; Mismatches 70; Indels 12; Gaps 3;
 QY 28 VEDMTDIOQSAPOTRLIITYWKDSEVRGLAVLSVSKSXSTLSCNKKIISFEEMDP 87
 DB 169 VYKYVDPSSQFKNPNGKVMGLGFTDPTLGVPASAVTGVEDTSLFTKNEFTFYDENQ 228
 QY 88 PENIDIOISDLFFOKRVPGHKNMEFESSLYEGHFLACQED-----DAFKLILKKK 139
 DB 229 PTFDALLSVASLNF---HNSIEAKD-YGTFIKISGSSIGENGMIVATKLTNFRK 284
 QY 140 DENGKSVMEFTLTN 153
 DB 285 DQGSRTMYPRAN 298
 RESULT 14
 ID 045916 PRELIMINARY; PRT: 1196 AA.
 AC 045916;
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE 138 KDA PROTEIN ASSOCIATED WITH BONT /C1-HAEMAGGLUTININ COMPLEX.
 GN CHN-138.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hauser D.F., Eklund M.W., Popoff M.R.;
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X66433; CAA47059.1;
 DR INTERPRO: IPR000395;
 DR PFAM: PF01742; Peptidase_M27; 1
 DR PRINTS: PR00760; BONTOTOXITYSTIN.
 DR PRODOM: PD001963; 1
 SQ SEQUENCE 1196 AA: 138725 MW: 88D5956301FA4A91 CRC64;
 Query Match 9.7%; Score 78; DB 2; Length 1196;
 Best Local Similarity 24.3%; Pred. No. 53;
 Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;
 QY 35 IDQASEPOTRLIITYWKDSEVRGLAV--TLVYKDSKXSTLSCNKKIISFEEMDPEN-- 90
 DB 965 ISISVRLKQDLIFT-NKKNVANSIDQILISTYSTINISLVKNKNSIYVELSVLDNPI 1023
 QY 91 -----IDDIQSDLIFFOKRVPGHKNMEFESSLYEGHFLACQEDDAFK 133
 DB 1024 TSEEVIIRNYFSYLDNSYIRDSKSLLEYKNKYOLYNYVFPETSLYE-----VNDNKSX 1077
 QY 134 LILKKDENGKSVMEFTLTNLOS 157
 DB 1078 LSLKNTDGINISSVKEFLINIDES 1101
 RESULT 15
 ID 053550 PRELIMINARY; PRT: 1196 AA.
 AC 053550;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 01, Last annotation update)
 DE PROGENITOR TOXIN L NONTOTOXIC-NONHEMAGGLUTININ COMPONENT (FRAGMENT).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96025415.
 RA Ohyama T., Watanabe T., Fujinaga Y., Inoue K., Sunagawa H., Fujii N.,
 RA Inoue K., Oguma K.;
 RT "Characterization of nontoxic-nonhemagglutinin component of the two
 RT types of progenitor toxin (M and L) produced by Clostridium botulinum
 RT type D CB-16."
 RL Microbiol. Immunol. 39:457-465(1995).
 DR EMBL: S80809; AAB36016.2;
 DR INTERPRO: IPR000395;
 DR PFAM: PF01742; Peptidase_M27; 1.
 FT NON_TER 1196 1196
 SQ SEQUENCE 1196 AA: 138717 MW: 6D2DBB5F6AF38324 CRC64;
 Query Match 9.7%; Score 78; DB 2; Length 1196;
 Best Local Similarity 24.3%; Pred. No. 53;
 Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;
 QY 35 IDQASEPOTRLIITYWKDSEVRGLAV--TLVYKDSKXSTLSCNKKIISFEEMDPEN-- 90
 DB 965 ISISVRLKQDLIFT-NKKNVANSIDQILISTYSTINISLVKNKNSIYVELSVLDNPI 1023
 QY 91 -----IDDIQSDLIFFOKRVPGHKNMEFESSLYEGHFLACQEDDAFK 133
 DB 1024 TSEEVIIRNYFSYLDNSYIRDSKSLLEYKNKYOLYNYVFPETSLYE-----VNDNKSX 1077
 QY 134 LILKKDENGKSVMEFTLTNLOS 157
 DB 1078 LSLKNTDGINISSVKEFLINIDES 1101

Search completed: November 21, 2000, 23:20:57
 Job time: 5083 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 17:23:54 : Search time 71.63 Seconds

(without alignments)
2470.154 Million cell updates/sec

Title: US-09-050-249-1

Perfect score: 471
Sequence: 1 AACTTGGCCGACCTCACTG.....TCACCTACTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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- 4: /cgn2_2/gcgdata/geneseq/geneseq/NA1983.DAT:*
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- 13: /cgn2_2/gcgdata/geneseq/geneseq/NA1992.DAT:*
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- 21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	99.9	471	17	T32403 Mouse interferon-g
2	470.6	99.9	471	17	T16224 Interferon gamma p
3	470.6	99.9	471	18	T60536 Mouse interferon-g
4	470.6	99.9	471	18	T80210 Murine protein for
5	470.6	99.9	471	19	V48227 Mouse interleukin
6	470.6	99.9	471	21	Z36923 DNA encoding a pro
7	470.6	99.9	570	19	V32755 Wild-type mouse in
8	469	98.6	471	19	V32633 Mutant mouse inter
9	467.4	99.2	471	19	V32632 Mutant mouse inter
10	400.6	85.1	722	19	V20875 Nucleotide sequenc
11	279.8	59.4	665	19	V20876 Nucleotide sequenc
12	268.4	57.0	582	21	Z55624 Equine interleukin

13	249.2	52.9	477	21	A10526 Human interleukin-
14	247.8	52.6	471	19	V48226 Human interleukin
15	247.8	52.6	471	19	V32625 Mutant human inter
16	247.8	52.6	471	19	V32626 Mutant human inter
17	247.8	52.6	570	19	V32754 Wild-type human in
18	247.8	52.6	1101	18	T74987 Interferon gamma 1
19	247.8	52.6	1101	18	T74987 Interferon gamma 1
20	247.8	52.6	1380	19	V05368 cDNA encoding huma
21	247.4	52.5	471	17	T32411 Human interferon-g
22	247.4	52.5	471	17	T32402 Human interferon-g
23	247.4	52.5	471	18	T80209 Human protein for
24	247.4	52.5	471	21	Z36875 DNA encoding a mat
25	247.4	52.5	579	19	V18906 Interferon-gamma 1
26	247.4	52.5	579	19	V17200 Interferon-gamma 1
27	247.4	52.5	1120	17	T32404 Human interferon-g
28	247.4	52.5	1120	19	V15825 cDNA for interfero
29	247.4	52.5	1120	21	Z36876 DNA encoding a pro
30	246.2	52.3	471	19	V33627 Mutant human inter
31	246.2	52.3	471	19	V33628 Mutant human inter
32	244.6	51.9	471	19	V48229 Human interleukin
33	244.6	51.9	471	19	V32628 Mutant human inter
34	244.6	51.9	471	19	V32630 Mutant human inter
35	244.4	51.9	540	20	X27732 Recombinant canine
36	244.4	51.9	540	21	A13801 Canine interleukin
37	244.4	51.9	582	20	X27724 Canine interleukin
38	244.4	51.9	582	21	A13793 Canine interleukin
39	244.4	51.9	582	21	Z55623 Canine interleukin
40	244.4	51.9	1427	20	X27726 Canine interleukin
41	244.4	51.9	1427	21	A13795 Canine interleukin
42	243	51.6	471	19	V48230 Human interleukin
43	243	51.6	471	19	V32631 Mutant human inter
44	127.8	27.1	11464	19	V48228 Interleukin 18 con
45	127.8	27.1	28994	19	V15826 Genomic DNA for in

ALIGNMENTS

RESULT	1
T32403	
ID	T32403 standard; cDNA to mRNA; 471 BP.
XX	
AC	T32403;
XX	
DT	29-SEP-1996 (first entry)
XX	
DE	Mouse interferon-gamma inducer protein cDNA.
XX	
KW	Interferon-gamma inducer; protein; IFN-gamma; antiviral; virucide;
KW	antitumour; antibacterial; immunoregulatory; adoptive immunotherapy;
KW	therapy; cancer; ds.
XX	
OS	Mus sp.
XX	
PN	EP12931-A2
XX	
PD	22-MAY-1996
XX	
PE	10-NOV-1995; 95EP-0308055.
XX	
PR	29-SEP-1995; 95JP-0274988.
PR	15-NOV-1994; 94JP-0304203.
PR	23-FEB-1995; 95JP-0058240.
PR	10-MAR-1995; 95JP-0078357.
PR	18-SEP-1995; 95JP-0262062.
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	
PI	Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
PI	Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX	
DR	WPI; 1996-252837/26.
DR	P-PDB; R99559.

XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders

PS Example A-3-2: Page 36-37; 48pp; English.

XX A cDNA clone (T32403) codes for a novel mouse protein (R99559) that
CC induces interferon-gamma (IFN-gamma) prodn. by immunocompetent cells.
CC The clone was obt'd. from a mouse liver cDNA library by PCR
CC amplification using primers (see also T32405-06) based on tryptic
CC peptides (R99561-62) of the protein. A DNA fragment based on
CC the cDNA clone was used to screen a human liver cDNA library,
CC leading to the isolation of a clone (T32402) coding for human mature
CC IFN-gamma inducer protein (R99558), a useful therapeutic agent.

XX Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.8e-124;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 AACTTGGCCGACTTCACTGATACACCGAGTAATACGAAATATAATGACCAAGTTCTC 60
DB 1 aactttggccgacttcaactgtacacacgcagatatacgaataataatgacccaagtctc 60
YY 61 TTGCTTGACAAAAGACAGCCTGTGTTGAGAGATATGACTGATATTAATCAAGTCCAGT 120
DB 61 ttgcttgacaaaagacagcctgtgttcgagagatattgactgatatatgataaagtccagt 120
YY 121 GAACCCAGACCGACTGATATATATCATCTACAAAGACGTAAGTAGAGAGCTGGCT 180
DB 121 gaacccagacccgactgataataatacatatgataaagacagtagaagaagacccgagct 180
YY 181 GTGACCCCTCTGTGAGAGATAGTAATAAAGTCTACCCCTCTCTGTAGAGAACAAAGATCATT 240
DB 181 gtgacccctctgtgagagatagtaataaagtctaccctctcgttagaagaacagatcatt 240
YY 241 TCCTTTGAGAAATGATGATCCACCTGAATAATATGATGATATACAAAGTATCTCATATTC 300
DB 241 tcctttgagaaatgatgattccacctgaataatattgatgatatataaagtgtccatattc 300
YY 301 TTTCAGAAAGCTGTTCCAGACACACAAAGATGAGATTGAATCTTCACTGATGAGGA 360
DB 301 ttccagaaagctgttccagacacacaaagatgagattgaattcaacttcacagtatgaaga 360
YY 361 CACTTTCTTGCTTGCAGAAAAGAGATGATGCTTTCAAACTCATTTGAAAAAAGAGAT 420
DB 361 cactttcttgcttgcagaaaagagatgatgctttcaaaactcatctcgaaaaaaagat 420
YY 421 GAAAAATGGGATTAATCTGTAATGTTTACTCTCTACTACTACTACTACTCAAAAT 471
DB 421 gaaaaatgggatataatctgtatgatttcaactcactcaactaactacaagt 471

RESULT 2

ID T16224 standard: cDNA to mRNA; 471 BP.

AC T16224;

DT 02-SEP-1996 (first entry)

DE Interferon gamma production inducer protein coding sequence.

XX Interferon gamma; inducer; IFN-gamma; immunocompetent cell; antiviral;
KM antitumor; antiseptic; immunoregulatory; platelet-increasing agent;
KM therapy; prevention; condyloma acuminatum; renal cancer; brain cancer;
KM granuloma; mycosis fungoides; rheumatism; allergy; cytotoxicity; AIDS;
KM killer T-cell; interleukin-2; IL-2; tumor necrosis factor; TNF;
KM adoptive immunotherapy; monoclonal antibody; ds.

OS Mus musculus.

PN EF692536-A2.

PD 17-JAN-1996.

PF 13-JUL-1995; 95EP-0304906.

PR 10-FEB-1995; 95JP-0045057.

PR 14-JUL-1994; 94JP-0184162.

PA (HAYB) HAYASHIBARA SEIBUTSU KAKAKU.

PI Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M,
PI Tanimoto T, Toriye K;

XX WPI: 1996-070177/08.

DR P-PSDB; R92506.

PT Protein that induces gamma interferon prodn. in immuno:competent
PT cells - used e.g. as antiviral or antitumor agent, also induces
PT cytotoxicity of killer cells

PS Claim 4; Page 22-23; 30pp; English.

This sequence represents the coding sequence for the interferon gamma
(IFN-gamma) inducer protein of the invention. The encoded protein induces
IFN-gamma production in immunocompetent cells. The protein is useful as
an antiviral, antitumor, antiseptic, immunoregulatory and
platelet-increasing agent. It can be used for treating or preventing
AIDS, condyloma acuminatum, renal or brain cancer, granuloma, mycosis
fungoides, rheumatism and allergy. The protein can also be used to
induce IFN-gamma production in cultured cells. The IFN-gamma inducer
strongly induces cytotoxicity of killer T-cells and when used with
interleukin-2 (IL-2) and tumor necrosis factor (TNF), may improve the
effect (or reduce side effects) of adoptive immunotherapy in tumors.
This sequence can be used to produce the protein, which can then be
purified (or assayed) using monoclonal antibodies.

SO Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.8e-124;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 AACTTGGCCGACTTCACTGATACACCGAGTAATACGAAATATAATGACCAAGTTCTC 60
DB 1 aactttggccgacttcaactgtacacacgcagatatacgaataataatgacccaagtctc 60
YY 61 TTGCTTGACAAAAGACAGCCTGTGTTGAGAGATATGACTGATATTAATCAAGTCCAGT 120
DB 61 ttgcttgacaaaagacagcctgtgttcgagagatattgactgatatatgataaagtccagt 120
YY 121 GAACCCAGACCGACTGATATATATCATCTACAAAGACGTAAGTAGAGAGCTGGCT 180
DB 121 gaacccagacccgactgataataatacatatgataaagacagtagaagaagacccgagct 180
YY 181 GTGACCCCTCTGTGAGAGATAGTAATAAAGTCTACCCCTCTCTGTAGAGAACAAAGATCATT 240
DB 181 gtgacccctctgtgagagatagtaataaagtctaccctctcgttagaagaacagatcatt 240
YY 241 TCCTTTGAGAAATGATGATCCACCTGAATAATATGATGATATACAAAGTATCTCATATTC 300
DB 241 tcctttgagaaatgatgattccacctgaataatattgatgatatataaagtgtccatattc 300
YY 301 TTTCAGAAAGCTGTTCCAGACACACAAAGATGAGATTGAATCTTCACTGATGAGGA 360
DB 301 ttccagaaagctgttccagacacacaaagatgagattgaattcaacttcacagtatgaaga 360
YY 361 CACTTTCTTGCTTGCAGAAAAGAGATGATGCTTTCAAACTCATTTGAAAAAAGAGAT 420
DB 361 cactttcttgcttgcagaaaagagatgatgctttcaaaactcatctcgaaaaaaagat 420

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471
 |||||||
 Db 421 gaaatgggataaactcgtactcactcactcactcaatcaagt 471

RESULT 3

ID T60536 standard: cDNA to mRNA: 471 BP.

AC T60536;

DT 26-JAN-1998 (first entry)

DE Mouse interferon-gamma inducer cDNA.

XX Interferon-gamma, IFN-gamma; antiviral; antitumour; radiotherapy;

KW immunoregulatory; antitumour agent; chemotherapy; leukaemia;

KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;

OS rheumatism; interleukin; killer cell; ds.

XX Mus musculus.

FT Key Location/Qualifiers
 mat_peptide 1..471
 /product= interferon gamma inducer

PN EP67178-A1.

PD 09-APR-1997.

PF 26-SEP-1996; 96EP-0306997.

PR 20-SEP-1996; 96JP-0269105.

PR 26-SEP-1995; 95JP-0270725.

PR 29-FEB-1996; 96JP-0067434.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;

DR WPI: 1997-205381/19.

DR P-PSDB: W15704.

PT Human protein that induces interferon-gamma prodn. in

PT immuno:competent cells - useful for adoptive immuno:therapy of

PT tumours and as antimicrobial agent etc.

XX Disclosure; page 22; 26pp; English.

XX The present sequence encodes a novel protein from mouse liver cells,

XX which induces interferon-gamma (IFN gamma) production in immunocompetent

XX cells. This protein enhances cytotoxicity of killer cells and induces

XX their formation. It is used as an antitumour agent for antitumour

XX immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,

XX and in the treatment of atopic or immune system diseases, e.g. asthma,

XX hayfever or rheumatism. When formulated with interleukin-3, it is also

XX used to treat leukaemia and thrombocytopaenia associated with

XX radiotherapy or chemotherapy of leukaemia and other cancers. When used

XX in antitumour immunotherapy, this novel protein significantly improves

XX the immunotherapeutic effect of interleukin-2 (IL-2), compared with use

XX of IL-2 alone, either when administered to the patient (before

XX administration of IL-2) or by addition to the medium in which cells

XX (intended for return to the patient) are being grown.

XX Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

XX Query Match 99.9%; Score 470.6; DB 18; Length 471;

XX Best Local Similarity 100.0%; Pred. No. 5,8e-124;

XX Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTGGCCGACTTACGTACACCGCAGTAATACGATATTAATGACCAAGTCTC 60
 |||||||
 Db 1 aacttggccgacttaccctgtacacccgcagtaatacagatataatgacccagttctc 60

OY 61 TTCGTTGACAAAAGACAGCCCTGTGTTGAGGATATGATATGATCAAGTCCAGT 120
 |||||||
 Db 61 ttcgttgacaaaagacagccctgtgttgagagatattgataatgataatgacagtgccagt 120

OY 121 GAACCCGACACGACTGATATATATATATATATATATATATATATATATATATAT 180
 |||||||
 Db 121 gaacccgacacgactgataataatataatataatataatataatataatataatataat 180

OY 121 gaacccgacacgactgataataatataatataatataatataatataatataatataat 180

OY 181 GTGACCCCTCTGTGAGAGATAGTAATAAGTCTACCTCTCTGTAAGACAGATCAT 240
 |||||||
 Db 181 gtgacccctctgtgagagatagtaataagctctacccctctgtaagacagatcat 240

OY 241 TCCCTTGGAGAAATGATCCACCTGAAATATGATATATATATATATATATATATAT 300
 |||||||
 Db 241 tcccttggagaaatgatccacctgaaatattgataataatataatataatataatataat 300

OY 301 TTTCAGAAAGCTGTTCAGACACACACACACACACACACACACACACACACACAC 360
 |||||||
 Db 301 tttcagaaagctgttcagac 360

OY 361 CACTTCTGCTTGCACAAAGAGATGATGCTTTCAACTCATTTGAAAAAAGAGAT 420
 |||||||
 Db 361 cacttctgcttgcacaaagagatgatgctttcaactcatTTGAAAAAAGAGAT 420

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471
 |||||||
 Db 421 gaaatgggataaactcgtactcactcactcactcaatcaagt 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

OY 421 GAAATGGGATAATCTGTAATGTCACCTCAGTACTACATCAAGT 471

PS Disclosure: Page 10-11; 12pp; Japanese.

XX This sequence encodes a protein which induces interferon-gamma
CC production in immunocompetent cells. This protein may be used as
CC the major component in a drug for the prevention and treatment of
CC e.g. malignant tumours, viral diseases, bacterial infections and
CC immune diseases.

XX Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

Query Match 99.9%; Score 470.6; DB 18; Length 471;

Best Local Similarity 100.0%; Pred. No. 5.8e-124; Indels 0; Gaps 0;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTTGGCCGACTCTGATGATACACGCGATATACGGAATATAATGACCAAGTTCTC 60
DB 1 Aactttggccgactctgactgatacaccgagtaataataatgaccaagttctc 60
OY 61 TTGCTTGACAAAAGACAGCCTGTGTCGAGGATATGACTGATTTGATCAAGTGCAGT 120
DB 61 ttcgcttgacaaaagacagcctgtgtcgaagataagactgataatgcaaaagtccagt 120
OY 121 GAACCCAGACGACGATATATATACATGTAACAAGACAGTGAAGAGAGACTGCGT 180
DB 121 gaacccagacgacgactgataataataataatgacaagactgaaagagactgct 180
OY 181 GTGACCCCTCTGTGAGGATAGTAAATGTCACCTCTCTGTAGAACAGATCATT 240
DB 181 gtgacccctctgtgagagtagtaaaagtctaccctctcctgtaagacaagatcatt 240
OY 241 TCCTTTGAGAAATGATCCACTGAAATATGATGATTAAGAATGATCCATATTC 300
DB 241 tcctttgagaaatgatccactgaaatattgatatatacaaaagtatcccatctc 300
OY 301 TTTCAGAAACGTGTCCAGACACAAACAGATGAGATTGTAATCTTCAGTATGAGGA 360
DB 301 tttcagaaacgtgttccagacacaaacagatgagattgtaattcttcacgtatgagga 360
OY 361 CACTTTCTGCTTCCCAAAAGAGATGATGTTTCAACTCATTTGAAAAAAGGAT 420
DB 361 cactttctgcttcccaaaagagatgattgtttcaactcatcttcgaaaaaaggat 420
OY 421 GAAATGGGATTAATGTGTAATGTTCACTGACTCACTTAATCATCAAGT 471
DB 421 gaaatgggataaattctgtcaatgctcactcaactcaatcaatcaagat 471

RESULT 5

ID V48227 standard: cDNA to mRNA; 471 BP.

XX V48227;

DT 16-NOV-1998 (first entry)

DE Mouse interleukin 18 gene.

XX Mouse; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia; ds;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KM chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

XX Mus sp.

OS Location/Qualifiers

XX Key 1..471

FT CDS /*tag- a

FT /product= "Interleukin 18"

PD /note= "No stop or start codon given"

EP861663-A2.

02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI: 1998-448964/39.

XX P-PSDB: w77078.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis

XX Disclosure: Page 29; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.

XX Sequence 471 BP; 162 A; 91 C; 92 G; 126 T; 0 other;

Query Match 99.9%; Score 470.6; DB 19; Length 471;

Best Local Similarity 99.8%; Pred. No. 5.8e-124; Indels 0; Gaps 0;

Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTTGGCCGACTCTGATGATACACGCGATATACGGAATATAATGACCAAGTTCTC 60
DB 1 Aactttggccgactctgactgatacaccgagtaataataatgaccaagttctc 60
OY 61 TTGCTTGACAAAAGACAGCCTGTGTCGAGGATATGACTGATTTGATCAAGTGCAGT 120
DB 61 ttcgcttgacaaaagacagcctgtgtcgaagataagactgataatgcaaaagtccagt 120
OY 121 GAACCCAGACGACGATATATATACATGTAACAAGACAGTGAAGAGAGACTGCGT 180
DB 121 gaacccagacgacgactgataataataataatgacaagactgaaagagactgct 180
OY 181 GTGACCCCTCTGTGAGGATAGTAAATGTCACCTCTCTGTAGAACAGATCATT 240
DB 181 gtgacccctctgtgagagtagtaaaagtctaccctctcctgtaagacaagatcatt 240
OY 241 TCCTTTGAGAAATGATCCACTGAAATATGATGATTAAGAATGATCCATATTC 300
DB 241 tcctttgagaaatgatccactgaaatattgatatatacaaaagtatcccatctc 300
OY 301 TTTCAGAAACGTGTCCAGACACAAACAGATGAGATTGTAATCTTCAGTATGAGGA 360
DB 301 tttcagaaacgtgttccagacacaaacagatgagattgtaattcttcacgtatgagga 360
OY 361 CACTTTCTGCTTCCCAAAAGAGATGATGTTTCAACTCATTTGAAAAAAGGAT 420
DB 361 cactttctgcttcccaaaagagatgattgtttcaactcatcttcgaaaaaaggat 420
OY 421 GAAATGGGATTAATGTGTAATGTTCACTGACTCACTTAATCATCAAGT 471
DB 421 gaaatgggataaattctgtcaatgctcactcaactcaatcaatcaagat 471

RESULT 6

ID Z36923 standard: cDNA to mRNA; 471 BP.

XX Z36923;

DT 13-MAR-2000 (first entry)

XX DNA encoding a protein that induces IFN-gamma production.

DE Mouse; interferon gamma production; IFN-gamma; immunocompetent cell;

XX antiviral; immunoregulatory; antigen; mitogen;

KW IFN-gamma susceptible disease; antibacterial; antitumor;

KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;

KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumor;

KW renal cancer; mycosis fungoides; chronic granulomatous disease;

KW blood cell malignant tumor; adult T cell leukemia;

KW chronic myelogenous leukemia; malignant leukemia; immune disease;

KW allergy; rheumatism; ds.

XX Mus sp.

XX key Location/Qualifiers

FT 1..471

FT mat_peptide /tag= a

FT /transl_except= (pos: 208..210, aa: Xaa)

FT /note= "Xaa is not specified"

XX EP962531-A2.

XX 08-DEC-1999.

XX 10-NOV-1995: 99EP-0104104.

XX 15-NOV-1994: 94JP-0304203.

XX 23-FEB-1995: 195JP-0058240.

XX 10-MAR-1995: 95JP-0078357.

XX 18-SEP-1995: 95JP-0262062.

XX 29-SEP-1995: 95JP-0274988.

XX 10-NOV-1995: 95EP-0308055.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Ushio S, Torigoe K, Tanimoto T, Okamura H;

XX WPI: 2000-064289/06.

XX P-PSDB: Y53905.

XX Novel polypeptides used in the treatment of interferon-gamma

XX susceptible diseases -

XX Disclosure: Page 3: 42pp; English.

XX PS The present sequence encodes a murine protein that induces interferon

XX CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a

XX CC protein which has antiviral, antitumor and immunoregulatory activities,

XX CC and is produced by immunocompetent cells stimulated with antigens or

XX CC mitogens. A probe derived from the present sequence was used to isolate

XX CC the corresponding human protein from human liver cells. The protein of

XX CC the invention is used to treat IFN-gamma susceptible diseases, and also

XX CC have use as an antiviral agent, antibacterial agent, antitumor agent,

XX CC immunoregulatory agent and blood platelet enhancing agent. Diseases

XX CC which can be treated with the protein include viral diseases, such as

XX CC hepatitis, herpes syndrome, condyloma, and AIDS; bacterial diseases

XX CC such as Candidiasis and malaria; solid malignant tumors such as renal

XX CC cancer, mycosis fungoides, and chronic granulomatous disease; blood

XX CC cell malignant tumors such as adult T cell leukemia, chronic

XX CC myelogenous leukemia, and malignant leukemia; and immune diseases

XX CC such as allergy and rheumatism.

XX SQ Sequence 471 BP; 162 A; 91 C; 92 G; 125 T; 1 other;

XX

Query Match 99.9%; Score 470.6; DB 21: Length 471;

Best Local Similarity 100.0%; Pred. No. 5.8e-124;

Matches 471: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACTTGGCCGACTTCTAGCAACGCGAGTAAATAGCAATGAAGCAAGTCTC 60

DB 1 aacttggccgacttctctgtacacgcagctatcagatataatgacccaagtcttc 60

OY 61 TTGCTGACAAAGACAGCCTGTGAGATATGATGATATGATCAAGTGCCACT 120

DB 61 ttcgttgacaaaagacagcctgttgagagatagactgatatgataaagtgccact 120

OY 121 GAACCCAGACAGCAGCTGTAATATACATGTACAAAGACAGTGAAGTAGAGACTGCT 180

DB 121 gaacccagacagcagctgtatatacatgatacaagaacagtgaaagtagactgct 180

OY 181 GTGACCCCTCTGTGAGATAGTAAAGTCTACCCCTCCTGTAAAGCAAGATCAT 240

DB 181 gtgacccctctgtgagatagtaaaagtgctaccctcctgttaagaacaagatcat 240

OY 241 TCCCTTGAGAAATGAGTACACCTGAAATATTGATATACAAAGTATCTCATTC 300

DB 241 tcccttgagaaatgagatcacctgaaatattgatatatacaagaatctcatctc 300

OY 301 TTTTCAGAAACGTGTTCCAGCACAACAAGATGAGCTTGAATCTTCACTGATGAGA 360

DB 301 ttctcagaacggttccagcacacaagaatgagcttgaatcttcaactgtatgaga 360

OY 361 CACTTCTTGCTTGCACAAAGAGATGATGCTTCAACATCATCTGAAAAAGAT 420

DB 361 cacttcttgcttgccaaagagatgattgcttcaacctcactcactcaactcataaagt 420

OY 421 GAAATGGGATTAATCTGTAATGTTCACTCTCACTAATCACTCACTCACTCACT 471

DB 421 gaaatgggataaatctgtatgttcaactcactcactcaactcataaagt 471

RESULT 7

V32755

ID V32755 standard; cDNA: 570 BP.

XX AC V32755:

XX DT 25-SEP-1998 (first entry)

XX DE Wild-type mouse interferon-gamma inducing factor cDNA.

XX KW Interferon-gamma inducing factor; interferon-gamma; killer cell;

XX KW antitumor agent; antiviral agent; antimicrobial agent; tumor; mGIF;

XX KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;

XX KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome; ds.

XX OS Mus sp.

XX FH key Location/Qualifiers

FT 1..15

FT 5'UTR /tag= a

FT CDS 16..558

FT /tag= b

FT /product= "Immature mouse IgG"

FT sig_peptide 16..84

FT /tag= c

FT /note= "This sequence claimed by the inventors

FT mat_peptide 85..555

FT /tag= d

FT 3'UTR 559..570

FT /tag= e

XX EP845530-A2.

XX 03-JUN-1998.

XX 28-NOV-1997: 97EP-0309632.

XX 14-NOV-1997: 97JP-0329715.

XX 29-NOV-1995: 96JP-0333037.

XX 21-JAN-1997: 97JP-0020906.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX	Kunimoto M,	Okamoto I,	Yamamoto K;
Pt	DR	WIPI:	1998-286747/26.
xx	DR	P-PSeD:	M48960.
xx	PT	Mutants of interferon-gamma inducing polypeptide - useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents	
PS	Claim 11;	pages 38-39;	59pp; English.
CC	The present sequence represents the wild-type mouse interferon-gamma inducing factor (mIGIF) cDNA. The invention provides for mutant mouse CC and human interferon-gamma inducing factors in which one or more CC cysteine residues are replaced with different residues at or away from CC the consensus sequences shown in W48956-W48958. The mutant mIGIFs are CC capable of stimulating immunocompetent cells for the production of CC interferon-gamma and are claimed to be less toxic, more active and stable than the corresponding wild type interferon-gamma inducing CC factor. The mutant mIGIFs are also claimed to enhance killer cell cytotoxicity and/or induce killer cell formation, and may therefore CC be useful as antitumour agents. Antitumour immunotherapeutics, antiviral CC agents and antimicrobial agents. The mutant mIGIFs are also claimed CC to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and thrombopenia caused by radiation- and chemo-therapy.		
SQ	Sequence 570 BP; 175 A; 123 C; 121 G; 151 T; 0 other;		
Oy	Query Match	99.9%; Score 470.6;	DB 19; Length 570;
Bst.Local Similarity	99.8%;	Pred. No. 6.2e-124;	
Matches 470;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0.
Dy	I AACTTTGGCGGACTTCAGCTACACGCATTAACGGAATTAAATGCCAAGTGTC TC 60		
Oy	61 TTGTGTTACAAGAAGCAGCAAGCTGTGGTAGAGATAATGCTCATATTCGCAAAGTCCAGT 120		
Dy	145 ttctgtgacaaaagacacgccttglttcgaaggatgatcgatatgtcatagtccagtt 204		
Oy	121 GAACCACGACGACAGCTGATTAATPAATGTTACAAAAGACAGTGAGTGAAGGACTGCT 180		
Dy	205 gaaccaccaaacagcacactgataataatgacaagaacagtagaaagagagctggct 264		
Oy	181 GTGACCCCTCTCTGTGAAGGATAGTAAAAAYGCTAACCCCTCCCTGTAAAGCAAGATCAT 240		
Dy	265 gtgacctcccctctgtgaaggatagtaaaaaatgctacccccctcccytaaagaagaataatt 324		
Oy	241 TTCCTTTGGGANAAGATCACCACTGAAAATTTGATGNATATACAAGTATCTCATATTC 300		
Dy	325 tcccttgtggagaaaygatgcccaactcgaaaataatlgatgatacaaaaygatcatactic 384		
Oy	301 TTTCGANAAGCTGTTCCAAGACACACAACAAGATGAGTTGAATCTTCACGTATGAAGGA 360		
Dy	385 tticcagaacgigtgccaggacacacacaagaatgagattlgaatctccocytgatygaaaga 444		
Oy	361 CACTTTCTTGTGTGGCAAAAGGAAGATATGCTTCAACACATCTTGAAAAAAGAGAT 420		
Dy	445 caattctctgtctgcgaaaaggaagaaaygatgctccaaccatctcigaaaaaaaaaagagt 504		
Oy	421 GAAATGGGAGTAATCTGTAATGTTCACTCTCACTAACTTACATCAAAAGT 471		
Dy	505 gaaaatggggataaatctcgtaatgtfccaactcctaacttacatcaaagt 555		
RESULT	8 V32633 standard; cDNA: 471 BP.		
V32633			
XX AC	V32633:		

XX	25-SEP-1998	(first entry)	
XX		Mutant mouse interferon-gamma inducing factor cDNA mIGIF/MUT12.	
XX		Interferon-gamma inducing factor; interferon-gamma; killer cell;	
KW		antitumour agent; antiviral agent; antimicrobial agent; tumour; mIGIF;	
KW		hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;	
KW		osteoporosis; thrombopenia; acquired immunodeficiency syndrome; ds.	
XX			
OS		Mus sp.	
OS		Synthetic.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..471	
FT		/*tag= a	
FT		/product= "mutant human interferon-gamma inducing	
FT		factor mIGIF/MUT12"	
FT		/note= "CDS does not contain a stop codon"	
FT	mutation	373..375	
FT		/*tag= b	
FT		/note= "changed from TGC in wild-type to AGC in	
FT		mutant"	
XX			
PN	EP845530-A2.		
XX			
PD	03-JUN-1998.		
XX			
PF	28-NOV-1997;	97EP-0309632.	
XX			
PR	14-NOV-1997;	97JP-0329715.	
PR	29-NOV-1996;	96JP-0333037.	
PR	21-JAN-1997;	97JP-0020906.	
XX			
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.		
PI			
PI	Kurimoto M, Okamoto I, Yamamoto K;		
XX			
DR	WPI: 1998-288747/26.		
DR	P-PSDB; W48969.		
XX			
PT	Mutants of interferon-gamma inducing polypeptide - useful as		
XX	antitumour, antiviral, antimicrobial or anti-immunopathic agents		
XX			
PS	Claim 10; page 50; 59pp; English.		
CC	The present sequence represents the mutant mouse interferon-gamma		
CC	inducing factor cDNA mIGIF/MUT12. The wild-type mouse interferon-gamma		
CC	factor (mIGIF) cDNA sequence is shown in V37755. The invention provides		
CC	for mutant human and mouse interferon-gamma inducing factors in which one		
CC	or more cysteine residues are replaced with different residues at or away		
CC	from the consensus sequences shown in W48956-W48958. The mutant mIGIFs		
CC	are capable of stimulating immunocompetent cells for the production of		
CC	interferon-gamma and are claimed to be less toxic, more active and		
CC	stable than the corresponding wild type mIGIF factor. The mutant mIGIFs		
CC	are also claimed to enhance killer cell cytotoxicity and/or induce killer		
CC	cell formation, and may therefore be useful as antitumour agents,		
CC	antitumour immunotherapeutics, antiviral agents and antimicrobial agents.		
CC	The mutant mIGIFs are also claimed to be useful for treating hepatitis,		
CC	acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid		
CC	malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and		
CC	thrombopenia caused by radiation- and chemo-therapy.		
XX			
SO	Sequence 471 BP; 163 A; 91 C; 92 G; 125 T; 0 other;		
QY	Query Match	99.6%; Score 469; DB 19; Length 471;	
QY	Best Local Similarity	99.6%; Pred. No. 1.6e-123;	
QY	Matches 469; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1 AACCTTGCCCACTTCACTGTACAACCGCAGTATACGATATTAATGACCAAGTTTCC 60		
QY	1 aactttgcccacttccactgtacaacccagtaataacgaataataatgaccaagtttcc 60		

DE	Nucleotide sequence encoding a rat interferon-gamma inducing factor	
KW	Rat interferon-gamma inducing factor; IGF; interleukin-18; IL-18;	
KW	IL-18-alpha; transformation; antibody; probe; hybridisation; ss.	
XX		
OS	Rattus sp.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..585
FT		/tag= a
FT	sig_peptide	/product= "interferon-gamma inducing factor"
FT		1..108
FT		/tag= b
XX		
PN	MO9810072-A1.	
PD	12-MAR-1998.	
XX		
PF	08-SEP-1997; 97MO-US15691.	
XX		
PR	08-APR-1997; 97US-0043087.	
PR	09-SEP-1996; 96US-0025141.	
XX		
PA	(CORR) CORNELL RES FOUND INC.	
XX		
PI	Conti B, Joh TH;	
XX		
DR	WPI; 1998-193622/17.	
DR	P-PSDB; W53282.	
XX		
PT	Rat interferon-gamma inducing factors and related DNA - useful for	
PT	quantitating stress in a mammal.	
XX		
XX	Claim 4; Page 31; 47pp; English.	
XX		
CC	This is the nucleotide sequence of the rat interferon-gamma inducing	
CC	factor (IGF), also known as interleukin-18 (IL-18). It can be used	
CC	to transform a cell, which upon its expression can cause the cell to	
CC	produce rat IGF, i.e. IL-18 or IL-18 alpha. The antibody to IGF,	
CC	IGF and probes derived from it, are useful for detection of IL-18	
CC	IL-18 alpha present in a sample. The amount of IL-18 or IL-18 alpha	
CC	in a sample can be used to quantitate stress in a mammal.	
XX		
XX		
XX	Sequence 722 BP; 252 A; 138 C; 140 G; 192 T; 0 other;	

Query Match	85.1%	Score	400.6	DB	19	Length	722
Similarity	91.8%	Pred. No.	4.1e-104				
Best Local							
Matches	434	Conservative	1	Mismatches	35	Indels	3
						Gaps	1

Oy	2	ACGTTGGCGAGCTCACTCATATACACCGAGATACGGAATTAAGGAATTAAGGACCAAGTCTCT	161
Db	110	actcttgacgactctcaactctgtacaaccgagtaatacgsagcataaatgaccaagtctctc	169
Oy	62	TCGTTGACAAAGA---CAGCCTGTGTTCGAGATATACGATGATTGATCAAAAGTCCCA	118
Db	170	tcgttgcacaaagaaccccgctgtgttcgtgaacatagcctgcatgcaccgaaacgcca	229
Oy	119	GTAACCCCGAGACACACATCATATATACATGTACAAGACAGTGAAGAGCACTGG	178
Db	230	acgaatcccgaccgacgactgtaatatatctgtacaagaatagtgaaagtaagagacttg	289
Oy	179	CTGTGACCCCTCTGTGAGAGGATAGTAAAAVCTACCCCTCCCTGATAGAACAAAGATCA	238
Db	290	ctgtgaccctcatctgtgaagaatgtgaagaaatgtcttaccctccctgtataaaaaaactca	349
Oy	239	TTTTCTTTGAGGAATGATTCACCCGGAATAATTGATGATATACAAAGTATCTCATAT	298
Db	350	ttctccttgsgaataatgaatccaccctggaataatattgattatataaagaatgactccat	409
Oy	299	TCTTTTCGAAGCGTTTCCGACGACACAAAGAATGAGTTTGAATCTTCACTGTATGAG	358
Db	410	tcttccagaacagtggtcccgagacatacaataaattgaaatttgaattcttccctgtatgag	465

Oy	359	GACACTTTCCTGCTTGCCAAAAGAAACATATAGCTTCGAACATCTCGAAAAAAGG	418
Db	470	gacattctctcgtctgcgcacaaaggaagatgactgtctcaacctcgtttgaagaagag	529
Oy	419	ATTGAATGGCGATTAATCTGTATATGTCCTCCACTAATCATACATCAAGT	471
Db	530	atgaataatggggatacaatctgtaatglttaactcttaacttaactacataaagt	582

RESULT	11
V20876	
ID	V20876 standard; cDNA; 665 BP
XX	
AC	V20876;

DE Nucleotide sequence encoding a rat interleukin-18-alpha.

Rat interferon-gamma inducing factor; IGF; interleukin-18; IL-18;
 IL-18-alpha; transformation; antibody; probe; hybridisation; ss.

OS Rattus sp.

key	Location/Qualifiers
FT	1..528
FT	/*tag= a
FT	/product= "interleukin-18-alpha"

PN W09810072-A1.

PD 12-MAR-1998

PF 08-SEP-1997; 97WO-US15891.

PR	08-APR-1997;	97US-0043087.
PR	09-SEP-1996;	96US-0025141.

PA (CORR) CORNELL RES FOUND INC.

Conti B, Joh TH

DR WPT; 1998-193622/17.
DR P-PSDB; W53283.

AA Rat interferon-gamma inducing factors and related DNA - useful for
PI quantitating stress in a mammal
PT

PS Claim 7; Pages 32-333; 47pp; English.

This is the nucleotide sequence of the rat interferon- γ inducible (IGIF) isoform, also known as interleukin-18- α factor (IL-18- α). It can be used to transform a cell, which upon its expression can cause the cell to produce rat IGIF, i.e. IL-18 or IL-18 α . It is made by the deletion of 57 bases (360-417) from V20875, a probable exon. The antibody to IGIF, IGIF and probes derived from it, are useful for detection of IL-18 or IL-18 α present in a sample. The amount of IL-18 or IL-18 α in a sample can be used to quantitate stress in a mammal.

Sequence 665, BP; 229 A; 130 C; 132 G; 174 T; 0 other;
AA
SQ

Query Match	59.4%	Score 279.8;	DB 19;	Length 655;
Best Local	80.1%	Pred. No. 5.5e-70;		
Matches 379; -Conservative	1;	Mismatches 33;	Indels 60;	Gaps 2

Oy 2 ACTTTGGCCGACTTCTACTGTACACCGCAGTAATACGAAATATAAAGACCAGAATTCTCI 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 actttggcagacttcactgtacacgcgagtaatcgtagataaalgaccagaattctct 169

Oy 62 TCGTTGCACAANAAG---CAGCCTGTGTTCGAGAGATGACTGATTAATGATCAAAAGTGCCA 118

```

Db 170 tccgtgacacaaagaaacccgcctgctgagagacatgcctatcgcgcgaacagcca 229
Oy 119 GTGAACCCAGACGACGATATATACATGTACAAAAGACAGTGAAGTAAGAGACTGG 178
Db 230 acgaatcccaagccagcagatataatataatgacaaagatagtaagaagaagactgg 289
Oy 179 CTGTGACCCCTCTCTGTGAAGATAGTAATAAAYGTCTACCTCTCTGTAGAACAGATCA 238
Db 290 cctgtagccctatctgtagagatgtagaagatgcttaccctcccgtaaaacaaata 349
Oy 239 TTTCTTTGAGGAATGATCCACTGAAATATTGATGATATACAAAGTATCTCATAT 298
Db 350 tttcctctg----- 358
Oy 299 TCTTTCAGAAAGCTGTTCAGGACACAAACAGATGAGTGTGATCTTCACTGATGAG 358
Db 359 -----agaaacgtgctgcagacacaaacaaatgaaattgaaattcctcgtatgaag 412
Oy 359 GACACTTCTCTGCTGCCAAAGAAAGATGATGCTTCAACTCTGAAAGAAAGG 418
Db 413 gacacttcttagctgccaagaaagatgcttcaactcgtttgaaaaggaag 472
Oy 419 ATGAAATGCGGATTAATCTGTAATGTTCTACTCTCACTACTTACATCAACT 471
Db 473 atgaaatgagggaataatctgtaactgctactactactactacatacaagt 525

```

RESULT 12

255624 255624 standard; cDNA; 582 BP.

AC 255624;

DT 27-MAR-2000 (first entry)

DE Equine Interleukin-18 (IL-18) cDNA.

Interleukin-18; IL-18; adjuvant; vaccine; immune reaction; equine; ss.

OS Equus caballus.

Key Location/Qualifiers

FT CDS 1..582

FT /tag= a

FT /product= "Equine IL-18"

XX W09956775-A1.

XX 11-NOV-1999.

XX 04-MAY-1999; 99WO-EP03098.

XX 07-MAY-1998; 98EP-0201451.

XX (ALKU) AKZO NOBEL NV.

XX Nicolson L, Rijske EO;

XX WPI; 2000-072212/06.

XX P-PSDB; Y58241.

XX Novel vaccine adjuvant used to increase the immune response

XX Claim 11; Page 22; 28pp; English.

CC This sequence represents cDNA encoding equine interleukin-18 (IL-18).
 CC The cDNA was produced from alveolar macrophage mRNA via reverse
 CC transcription using primer 255625, and the cDNA amplified via PCR using
 CC primers 255626-255629. The invention relates to the use of recombinant
 CC IL-18 as a vaccine adjuvant. Adjuvants are used in vaccines to
 CC potentiate the immune response to an antigen derived from the pathogen.
 CC It is important that the correct type of immune reaction is triggered,

CC since many types of immune mechanisms that can be activated are
 CC inadequate for the control of a particular pathogen. Mice were injected
 CC intramuscularly with a vaccine formulation either containing inactivated
 CC pseudorabies virus (PRV) plus tetanus toxoid (TT), or a formulation
 CC containing inactivated PRV, TT and 0.1 micrograms of recombinant murine
 CC IL-18. When subsequently challenged with virulent PRV, unvaccinated
 CC control mice all succumbed to the infection, and only 30% of mice
 CC vaccinated with vaccine antigen alone (inactivated PRV plus TT) survived
 CC the infection. In contrast, mice which received the same amount of
 CC vaccine antigen in conjunction with IL-18 had an 80% survival rate
 CC after infection. IL-18 may be used as an adjuvant in vaccines for the
 CC immunisation of humans and other animals, such as pigs, sheep, birds,
 CC cattle, dogs, horses and fish. An adjuvant composition comprising
 CC IL-18 may be administered concomitantly or sequentially with a vaccine
 CC formulation. Additionally, IL-18 nucleotides operably linked to
 CC transcriptional regulatory sequences may be used in DNA vaccines for the
 CC in vivo expression of IL-18 in the cells of a vaccinated animal.

Sequence 582 BP; 200 A; 102 C; 113 G; 167 T; 0 other;

Query Match 57.0%; Score 268.4; DB 21; Length 582;
 Best Local Similarity 76.5%; Pred. No. 8.8e-67;
 Matches 355; Conservative 1; Mismatches 102; Indels 6; Gaps 2;

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Oy 2 ACTTTGGCGGCACTTCATCTGTACACCGAGTAATACGAAATTAATGACCAAGTCTCT 61
Db 110 actttggcgaggttgaactaaactcaatcatcagaatttgacgacgaagttctct 169
Oy 62 TCGTTGACAAAGA--CAGCCTGTGTTGAGGATATGACTATTTGATCAAAAGTGCA 118
Db 170 tcaataaccaggaagaaatacaacctgcttgaagataatcgtctctgatttacaagaca 229
Oy 119 GTGAACCCAGACGACGATATATACATGTACAAAGACAGTGAAGTAAGAGACTGG 178
Db 230 acgcaccccaagacgattatcatatataatgataaagatagctcactagaagttcag 289
Oy 179 CTGTGACCCCTCTCTGTGAAGATAGTAATAAAYGTCTACCTCTCTGTAGAACAGATCA 238
Db 290 cgttaacctctctgtagaagtgtagaagaaacgtctcaactctcccgtaagaacaaatla 349
Oy 239 TTTCTTTGAGGAATGATCCACTGAAATATTGATGATATACAAAGTATCTCATAT 298
Db 350 tttcctttaaagaaatgcttccctcgtagaataatgaaagaaatgacatcata 409
Oy 299 TCTTTCAGAAAGCTGTTCAGGAC--ACAACAAGATGAGTGTGAACTTCACTGATG 355
Db 410 tcttcagagaagtgctccagacatgataagatacagtttgagttcttcactgata 469
Oy 356 AAGGACACTTCTTCTGCCAAAGAAAGATGATGCTTCAACTCTGAAAGAAANA 415
Db 470 aaggatacttcttagctgtagaagaaagaaatgatacttccaactcatcttggaaagaa 529
Oy 416 AGGATGAATGCGGATTAATCTGTAATGTTCTACTCTCACTCACTAAC 459
Db 530 aggatgaaatggggataaatctgtaactgctacactgcttcaaac 573

```

RESULT 13

A10526 10526 standard; cDNA; 477 BP.

AC A10526;

DT 23-JUN-2000 (first entry)

DE Human Interleukin-18 (IL-18) nucleotide sequence.

Interleukin-18; production; IL-18; human; ss; medical injection product.

OS Homo sapiens.

XX CN1243130-A.

stable than the corresponding wild type interferon-gamma inducing factor. The mutant IGFs are also claimed to enhance killer cell cytotoxicity and/or induce killer cell formation, and may therefore be useful as antitumour agents, antitumour immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and thrombopenia caused by radiation and chemo-therapy.

XX
Sequence 471 BP, 166 A; 78 C; 87 G; 140 T; 0 other:

XX

Query Match	52.6%	Score 247.8	DB 19	Length 471
Best Local Similarity	73.3%	Prod. No. 5.4e-61		
Matches 344	Conservative 1	Mismatches 118	Indels 6	Gaps 2
2	ACTTGGCCGACTCAGCTACAAACCCGAGTAATCGGAAATATAATACCAAGTTCTCT	61		
1				
2	actttggaaagcttgaacttaataatcatagtcataagaacttgaatgaaccagttcct	61		
62	TCGTTGACAAAAGACA--GCCGTGTTCGAGATATGACTGATATGATCAAAAGTGCCA	118		
1				
62	tcattgaccagaagaatcgccctatttgaagatagatgacttctgactgtagagata	121		
119	GTGAACCCCAACCAAGATGTGATTAATATACATGTACAAAGACGTAAGTAAGAGACTGG	178		
1				
122	atgaccccccgaacatattatataaagatgataaagaatagccagccctgaaggtatgg	181		
179	CTGTGACCCCTCTGTGTGAAGGATAGTAAATGTATACCTCTCCTGTAAAGACAGATCA	238		
1				
182	ctgtaaccatctctgtgtaagtcctgagaataattcaacctctccctgtagaacaata	241		
239	TTTCTTTGAGGAATGAGATCCACCTGGAATATTGATGATATACAAAGTGAATCTCAT	298		
1				
242	tttcctttaaggaatgatctcctctgtataacatcaagatacaaaaagtgcattcat	301		
299	TCTTTCAGAAACGTTGTCAGAGAC--ACAACAGATGAGATTGAATCTTACCTGTATG	355		
1				
302	tcttcagaagaagtcctccagaacatgataataaagatgcaatttgaatcttcata	361		
356	AAGGACACTTTCCTGCTGTCGCAAAAGAAAGATGATGCTTTCAAACTCATTTGAA	415		
1				
362	aaggtactcttctagcttgtagaaaagagagagagaccttctaactcatlttgaaa	421		
416	AGGATGAATATGGGATTAATCTGTAATGTTTCACCTCTCATACTTACACTTACA	464		
1				
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Wed Nov 22 11:24:54 2000

us-09-050-249-1.rng

Page 12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 17:19:13 ; Search time 61.39 Seconds
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Title: US-09-050-249-1

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Sequence: 1 AACCTGGCCGACTACTG.....TCACTACTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	470.6	99.9	471	4	US-08-908-005A-1 Sequence 1, Appli
3	247.4	52.5	579	3	US-08-896-605A-7 Sequence 7, Appli
4	247.4	52.5	579	3	US-08-896-501A-5 Sequence 5, Appli
5	247.4	52.5	1120	5	US-08-884-324-2 Sequence 2, Appli
6	127.8	27.1	1164	5	US-08-884-324-13 Sequence 13, Appli
7	127.8	27.1	28994	5	US-08-884-324-14 Sequence 14, Appli
8	122	25.9	2167	5	US-08-884-324-7 Sequence 7, Appli
9	75.6	16.1	134	5	US-08-884-324-4 Sequence 4, Appli
10	51.4	10.9	135	5	US-08-884-324-3 Sequence 3, Appli
11	38.4	7.8	7218	1	US-08-332-463-14 Sequence 14, Appli
12	36.8	7.2	4731	5	US-08-488-706-2 Sequence 2, Appli
13	36.8	7.8	4731	5	US-08-772-270A-9 Sequence 9, Appli
14	34.4	7.3	10614	1	US-08-135-511-35 Sequence 35, Appli
15	34.4	7.3	10614	2	US-08-187-453-35 Sequence 35, Appli
16	33.8	7.2	8920	3	US-08-446-855A-1 Sequence 1, Appli
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31	30.4	6.5	14602	2	US-08-597-236-1 Sequence 1, Appli
32	30.4	6.5	14602	2	US-08-746-682A-1 Sequence 1, Appli
33	29.8	6.3	5035	4	US-08-616-392C-3 Sequence 3, Appli
34	29.6	6.3	26700	2	US-08-472-217-1 Sequence 1, Appli
35	29.6	6.3	26700	3	US-08-488-199-5 Sequence 5, Appli
36	29.6	6.3	26700	3	US-08-760-534A-1 Sequence 1, Appli
37	29.2	6.2	1600	5	US-09-028-819-14 Sequence 14, Appli
38	29.2	6.2	5033	1	US-08-038-768A-1 Sequence 1, Appli
39	29	6.2	3515	3	US-08-391-743A-1 Sequence 1, Appli
40	28.8	6.1	1837	4	US-08-909-965C-10 Sequence 10, Appli
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44	28.8	6.1	3634	5	US-09-166-186-1 Sequence 1, Appli
45	28.8	6.1	3792	4	US-08-992-334-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-502-535B-1
Sequence 1, Application US/08502535B
Patent No. 5912324

GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakui
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IEN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502.535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
FAX: 202-737-3528
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..471
OTHER INFORMATION: /note= Xaa in position 70 is Met or Thr
US-08-502-535B-1

Query Match 99.9%; Score 470.6; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.4e-132;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGGCCGACTTCACTGATCAACCCGACGATATACGGAATATAAGCAAGTCTTC 60
DB 1 AACCTGGCCGACTTCACTGATCAACCCGACGATATACGGAATATAAGCAAGTCTTC 60
QY 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATATGATGATATGATCAAGTCCAGT 120
DB 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATATGATGATATGATCAAGTCCAGT 120
QY 121 GAACCCAGACGACGATGATATATATATATATATATATATATATATATATATAT 180
DB 121 GAACCCAGACGACGATGATATATATATATATATATATATATATATATATATAT 180
QY 181 GTGACCTCTCTGTGATGATATGATATATATATATATATATATATATATATAT 240
DB 181 GTGACCTCTCTGTGATGATATGATATATATATATATATATATATATATATAT 240
QY 241 TCCCTTGAGAAATGATATGATATATATATATATATATATATATATATATATAT 300
DB 241 TCCCTTGAGAAATGATATGATATATATATATATATATATATATATATATATAT 300
QY 301 TTTCGAAACGCTGTCGAGACACACAAAGATGAGATTGATATATATATATATAT 360
DB 301 TTTCGAAACGCTGTCGAGACACACAAAGATGAGATTGATATATATATATATAT 360
QY 361 CACTTCTTGCTTGGCAAAAGAGATGATGCTTTCAAACTCATCTGAAAAAAGAT 420
DB 361 CACTTCTTGCTTGGCAAAAGAGATGATGCTTTCAAACTCATCTGAAAAAAGAT 420
QY 421 GAAAAATGGGATAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471
DB 421 GAAAAATGGGATAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471

RESULT 2
US-08-908-005A-1
Sequence 1, Application us/08908005A
Patent No. 5914253

GENERAL INFORMATION:

APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKUCHI, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,005A
FILING DATE: 11-AUG-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/502,535
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROMDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..471
OTHER INFORMATION: /note= Xaa in position 70 is Met or Thr
US-08-908-005A-1

Query Match 99.9%; Score 470.6; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.4e-132;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTGGCCGACTTCACTGATCAACCCGACGATATACGGAATATAAGCAAGTCTTC 60
DB 1 AACCTGGCCGACTTCACTGATCAACCCGACGATATACGGAATATAAGCAAGTCTTC 60
QY 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATATGATGATATGATCAAGTCCAGT 120
DB 61 TTCGTTGACAAAGACAGCCTGTGTCGAGATATGATGATATGATCAAGTCCAGT 120
QY 121 GAACCCAGACGACGATGATATATATATATATATATATATATATATATATATAT 180
DB 121 GAACCCAGACGACGATGATATATATATATATATATATATATATATATATATAT 180
QY 181 GTGACCTCTCTGTGAGATAGTAAATGTCACCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GTGACCTCTCTGTGAGATAGTAAATGTCACCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 TCCCTTGAGAAATGATGATATATATATATATATATATATATATATATATATAT 300
DB 241 TCCCTTGAGAAATGATGATATATATATATATATATATATATATATATATATAT 300
QY 301 TTTCGAAACGCTGTCGAGACACACAAAGATGAGATTGATATATATATATATAT 360
DB 301 TTTCGAAACGCTGTCGAGACACACAAAGATGAGATTGATATATATATATATAT 360
QY 361 CACTTCTTGCTTGGCAAAAGAGATGATGCTTTCAAACTCATCTGAAAAAAGAT 420
DB 361 CACTTCTTGCTTGGCAAAAGAGATGATGCTTTCAAACTCATCTGAAAAAAGAT 420
QY 421 GAAAAATGGGATAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471
DB 421 GAAAAATGGGATAATCTGTAATGTTCACTCTCACTAATCAATCAAGT 471

RESULT 3
US-08-896-605A-7

Sequence 7 Application US/08896605A
Patent No. 5879942

GENERAL INFORMATION:

APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO. 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: leader peptide
LOCATION: 1..108
IDENTIFICATION METHOD: S
NAME/KEY: mat peptide
LOCATION: 109..579
IDENTIFICATION METHOD: S

US-08-896-605A-7

Query Match	52.5%: Best Local Similarity	73.1%: Conservative	Procd 247.4: Mismatches	DB 3: Indels	Length 579: Gaps
QY	2	ACTTTGGCCGACTTCACTGTACCAACCCAGTAATACGAATATATAATGACCAATTCTCT	61		
Db	110	ACTTTGGCCAGCTTGATCTTAATATTACAGCATATACAAATTTGAATGACCAAGTTCTCT	169		
QY	62	TCGTTGACAAAAGCA---GCCGTGTTCGAGGATTCAGCTGATATGATCAAAAGTCCCA	118		
Db	170	TCATTTGACCAAGGAATCGGCCCTTATTTTGACATATGACCTGATTTCTGACTGTAGAGATA	229		
QY	119	GTGACCCCCAGACCAGACTGATAATATACATGTACCAAGACAGTGAATAGAGAGACTGG	178		
Db	230	ATGCACCCCGGACCATTTTATTATTAGTATGTATTAAGATATAGCCAGCTTAGAGATATGG	289		
QY	179	CTGTGACCCCTCTCTGTGTAGAGATGTAAAYGTGTACCCTCTCCTGTAAACAAAGATCA	238		
Db	230	CTGTACATCTCTGTGTAGAGGTAGAAAATTTCAATCTCTCTGTGTGAAACAAATTA	349		
QY	239	TTTCCCTTTGAGGAATGGATCCACCTGAATAATATTGATATATACAAAGTGAATCTCATAT	298		

Db 350 TTTCTTAAAGGAATATAATCTCTCTATATAACTCAAGGATACAAAAAGGACATCATAT 409
QY 299 TCTTTTCGAAGACGTGTCCAGAGAC--ACAACAAGATGAGGTTGAATCTTCACGTGTATG 355
Db 410 TCTTTCAGAGAGAGTGTCCAGAGCATATATATAGATGCAATTGGATCTTCATCATAGC 469
QY 356 AAGGACACTTCTTGCTTGCCAAAAGGAGATGATGCTTTCAACATCTGTGAAAAAAA 415
Db 470 AAGGATACCTTCTAGCTTGGAAGAAAAGAGAGAGACCTTTTAAACTATTTTGAAAAAG 529
QY 416 AGGATGAAATGGGATATAATCTGTAAATGTTCACCTCTCACTAACTTACA 464
Db 530 AGGATGAAATGGGATAGATCTTAATATGTTCACTGTTCAAAAGGAAGA 578

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RESULT 4
US-08-896-501A-5
: Sequence 5, Application US/08896501A
: Patent No. 5891663
: GENERAL INFORMATION:
: APPLICANT: TANIMOTO, Tadao
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/896,501A
: FILING DATE: 18-JUL-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 213,267/1996
: FILING DATE: 25-JUL-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 31,474/1997
: FILING DATE: 31-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: TANIMOTO-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: leader peptide
: LOCATION: 1..108
: IDENTIFICATION METHOD: S
: NAME/KEY: mat peptide
: LOCATION: 109..579
: IDENTIFICATION METHOD: S
US-08-896-501A-5
Query Match 52.5% Score 247.4; DB 3; Length 579;
Best Local Similarity 73.1%; Pred. No. 2.4e-65;
Matches 343; Conservative 2; Mismatches 110; Indels 6; Gaps 2

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1      LENGTH: 1120 base pairs
2      TYPE: nucleic acid
3      STRANDEDNESS: double
4      TOPOLOGY: linear
5      MOLECULE TYPE: cDNA to mRNA
6      HYPOTHETICAL: No
7      ANTI-SENSE: No
8      ORIGINAL SOURCE:
9      ORGANISM: human
10     TISSUE TYPE: liver
11
12     FEATURE:
13     NAME/KEY: 5'UTR
14     LOCATION: 1..177
15     IDENTIFICATION METHOD: E
16     NAME/KEY: leader peptide
17     LOCATION: 178..285
18     IDENTIFICATION METHOD: S
19     NAME/KEY: mat peptide
20     LOCATION: 286..756
21     IDENTIFICATION METHOD: S
22     NAME/KEY: 3'UTR
23     LOCATION: 757..1120
24     IDENTIFICATION METHOD: E
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26     US-08-884-324-2
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Query Match Similarity 52.5%; Score 247/4; DB 5; Length 1120;
Best Local Similarity 73.1%; Pred. No. 3,2e-65;
Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2;

Dy 2 ACTTTGGCCGACTCAGCTGATACACCAGCAATCGCATTCGTAAATTAATGACCAAGTTCCT 61
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 AATTGGGACAGCTTAATICTAATATTATATGATCATAGAATAATTGAATGCCAAGTTCCT 346
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 62 TCGTTGACAAAAAGACA---GCCTGTGTTGAGAGATATGACTGATATTTGATCAAAGTGCCA 118
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 TCATTGACCAAGGAATCGCCTCTATTGTAAGATATGACTGATTCCTGACTGTAGAGATA 406
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 119 GTGAACCCCACAGCACGACTGATAATATACATCTACAAAAGCAGTGAAGTAAGAGACAGG 178
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 407 ATGCACCCCCGACCACTATTATTATTAAGTAGTATAAAGATAGCCAGCCCTAGAGTATGG 466
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 179 CTGTACCCCTCTCTGTGAAGATAGTAATAAAYGTCTACCCCTCTCTGTAGAACAAGATCA 238
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 467 CGTGACTATCTCTGTGAAGTGTAGAAATTTCAAATCTCTGCTGTGAGAACAAATTA 526
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 239 TTTCCTTTGAGAAATGATGCCACTGAAATATTGATGATATACAAAAGTATTCATAT 298
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 527 TTTCCTTTAAGAAATGAATCCTCTGTATACATCAAGATATCAAAAAGTGACATCATAT 586
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 299 TCTTCAGAAAGSTTCCAGAGC---ACAACAAGATGAGTTGAATCTTCACTGTATG 355
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 587 TCTTCAGAGAGTGTCCAGSACATGATATAAAGATGCAATTTGATCTTATCATACAG 646
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 356 AAGGACACTTTCCTGCTGCCAAAAGGAAGATGATGCTTCAACTCATTTGAAAAAAA 415
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 647 AAGGATACTTCTACTGTGTGA AAAAGAGAGAGACCTTTTAAACTCATTTTGA AAAAAG 706
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 416 AGGATGAATAATGGGATAAATCTGTAATGTTACTCTCACTACTTAC 464
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 707 AGGATGAATGGGGATAGATCTATTAATGTTCACTGTTCAAAACAGAGA 755
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-08-884-324-13
Sequence 13, Application US/080884324
Patent No.: 6060283
GENERAL INFORMATION:
APPLICANT: Takanoji OKURA
APPLICANT: Kakuji TORIOE
APPLICANT: Masahi KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-

NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NETMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 City: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/984,324
 APPLICATION DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 185,305/96
 FILING DATE: 27-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: OKURA-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11464 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: human
 TISSUE TYPE: placenta
 FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: 1..3
 IDENTIFICATION METHOD: E
 NAME/KEY: leader peptide
 LOCATION: 4..82
 IDENTIFICATION METHOD: S
 NAME/KEY: intron
 LOCATION: 83..1453
 IDENTIFICATION METHOD: E
 NAME/KEY: leader peptide
 LOCATION: 1454..1465
 IDENTIFICATION METHOD: S
 NAME/KEY: intron
 LOCATION: 1466..4848
 IDENTIFICATION METHOD: E
 NAME/KEY: leader peptide
 LOCATION: 4849..4865
 IDENTIFICATION METHOD: S
 NAME/KEY: mat peptide
 LOCATION: 4866..4983
 IDENTIFICATION METHOD: S
 NAME/KEY: intron
 LOCATION: 4984..6317
 IDENTIFICATION METHOD: E
 NAME/KEY: mat peptide
 LOCATION: 6318..6451
 IDENTIFICATION METHOD: S
 NAME/KEY: intron
 LOCATION: 6452..11224
 IDENTIFICATION METHOD: E
 NAME/KEY: mat peptide
 LOCATION: 11225..11443
 IDENTIFICATION METHOD: S
 NAME/KEY: 3'UTR
 LOCATION: 11444..11464

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IDENTIFICATION METHOD: E
US-08-884-324-13

Query Match          27.1% Score 127.8; DB 5; Length 11464;
Best Local Similarity 73.3%; Pred. No. 6,7e-29;
Matches 178; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

OY 225 TAAGACACAGATCATTTCTCTTGAGGAAATGATCCACCTGAAATATTGATGATATACA 284
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11200 TTAGTATATGTTTTTTTCTCTATAGGAATGAATCCTCTGTATACATCAGAGATACAA 11259

OY 285 AAGTATCTCATTTATCTTCTTCAGAAACGTTGCCAGAC---ACACAGATGGAGTTTGA 341
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11260 AAGTACATCATATTTCTTTCAGAGAGTGTCCTCCAGACATGTAATTAAGATGCAATTGA 11319

OY 342 ATCTTCACGTATGAGAGACACTTTCCTTGCTTGCCAAAGAGATGATGCTTCAACT 401
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11320 ATCTTCATCATACGAGAGATTACTTCTAGCTTGTAAGAAAGAGACACTTTTAACT 11379

OY 402 CATTTGAAAAAAGATGAATAATGGGATTAATCTGTAATGTTCACTCTACTACTT 461
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11380 CATTTGAAAAAAGAGATGAATTGGGGATATGATCTAATATGTTCACTGTTCAAAAGCA 11439

OY 462 ACA 464
      |||
Db 11440 AGA 11442

RESULT 7
US-08-884-324-14
Sequence 14, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahiko KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA

```


APPLICANT: TAKAMORI OKURA
APPLICANT: KAKUJI TORIGOE
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: exon
LOCATION: 1..135
IDENTIFICATION METHOD: S

US-08-884-324-3

Query Match 10.9% Score 51.4; DB 5; Length 135;
Best Local Similarity 70.9%; Pred. No. 8.2e-07;
Matches 83; Conservative 0; Mismatches 31; Indels 3; Gaps 1

OY 2 ACTTTGCCGAGCTTCACTGTACACCGCATTAATACGAATAAATGCACAAGTTCCT 61
 ||||| | | | | | | | | |
DB 19 ACTTGCCAGAGCTTAATCTAAATATATCAGCATFAAGAATTTGGATGACCAGTTCCT 78
 ||||| | | | | | | | | |

OY 62 TCGTTGACAAAAGACA--GCCTGTGTTGCGAGGATATGACTATATGTATCAAAAGTG 115
 . ||||| | | | | | | | | |
DB 79 TCATTGACCAAGGAATCGGCCTCTATTGAGATATGACTGATTCTGACTGTAGAG 135
 . ||||| | | | | | | | | |

RESULT 11:
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNBER, F.
APPLICANT: SCHEIFFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOULPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F15
US-08-232-463-14

Query Match 8.2%; Score 38.4; DB 1; Length 7218;
Best Local Similarity 8.1%; Pred. No. 0.036;
Matches 36; Conservative 207; Mismatches 203; Indels 0; Gaps 0;
OY 11 GACTTACTGTGACACCGCATATACGGAATATAATGACCAAGTCTCTGTTGACA 70
DB 1492 GGCATCACTGATATATGCTATCTATGCAAGTAAAGAGATAGAGATTGTGACR 1433
OY 71 AAGACACGCTGCTGTCAGAGATAGCATGATATGATCAAGTGCACGAGACCCACA 130
DB 1432 RR 1373
OY 131 CGACTGATATATACATGATACAAAGACAGTAGAAGAGACGCTGAGACCTCT 190
DB 1372 RR 1313
OY 191 CTGGAAGATAGTAAAVGTACCTCTCTGTAAGAACAGATCAATTCCTTTGAGG 250
DB 1312 RR 1253
OY 251 AATGATCCACCTGAAATATGATGATATACAAAGTATCTCATATCTTTCACAAC 310
DB 1252 RR 1193
OY 311 GTGTCAGACACACAAAGATGAGTTGAATCTTCAGTATGAAGACACTTCTTG 370
DB 1192 RR 1133
OY 371 CTGCAAAAGAGATGATGCTTCAACTCAATCTGAAAAAAGATGAATAGGGG 430
DB 1132 RR 1073
OY 431 ATAATCTGTAATGCTGCTCACT 456

DB 1072 RRRRRRATCCAGCTCCTGACCT 1047
RESULT 12
US-08-488-706-2
Sequence 2, Application US/08488706
Patent No. 5994525
GENERAL INFORMATION:
APPLICANT: Kamp, Elbarte M.
TITLE OF INVENTION: Recombinant Vaccine For Prevention and/or
TITLE OF INVENTION: Treatment of Pleuropneumonia Infections
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abdelman, Freyne & Schwab
STREET: 708 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC or compatible
OPERATING SYSTEM: DOS 3.31
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488.706
FILING DATE: 09-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/722.971
FILING DATE: 28-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cinnamon, Jay S.
REGISTRATION NUMBER: 24,156
REFERENCE/DOCKET NUMBER: 201,875
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-949-9190
TELEFAX: 212-949-9022
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4731
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-488-706-2
Query Match 7.8%; Score 36.8; DB 4; Length 4731;
Best Local Similarity 47.4%; Pred. No. 0.091;
Matches 110; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
OY 211 TCTACCTCTCTGTAAGAACAGATCATTTCTTGGAGAAATGATCCACTGAAAT 270
DB 591 TCTATCTAGCAAAAAGATGCTGAAAATCATATATTAAAGAGGAAAATATACAA 650
OY 271 ATTGATGATATACAAAGTATGCTATGCTTTCAGAAAGTCTTCCAGGACCAACAG 330
DB 651 AAAAGTAGCTGAAAGACATTTCTTCAAGTATGAGCAAGAGTATTAACAGCTCAAT 710
OY 331 ATGAGTTGATCTTCACTGATATGAGGACACTTCTTCTGCCCCAAAAGAGATGAT 390
DB 711 AATATCTTAATGATGATATATATAAAGAGACTCTTTATGTCAAAAATCACTTGTG 770
OY 391 GCTTCAATCATTTCTGAAAAAAGATGAAATGAGGATAATGCTAA 442
DB 771 ATCATTAATATGCTTACACAAAGATGAAAAAAGGAAAAAACAAGTTA 822
RESULT 13
US-08-772-270A-9
Sequence 9, Application US/08772270A
Patent No. 6019984

3aps	0;
T 288	

A 10191

A 348
A 10131

408

TJ 10071

t

015

5

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2000, 16:55:18 : Search time 399.28 Seconds
(without alignments)
7293.383 Million cell updates/sec

Title: US-09-050-249-1

Perfect score: 471
Sequence: 1 AACTTGGCCGACTCCTG.....TCACACTTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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123: em_gss12: *
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126: em_gss15: *
127: em_gss16: *

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Result No.	Score
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No.	Score	Query Match	Length	DB	ID	Description
1	465.8	98.9	603	7	AA930362	AA930362 v559i07.t
2	400.6	85.1	646	7	AA892285	AA892285 EST196088
3	365.6	77.6	512	20	AM125102	AM125102 UI-M-BH2
4	337.6	71.7	474	8	AI120720	AI120720 u699c02.x
5	308.6	65.5	434	2	AA237736	AA237736 m329q01.t
6	274	58.2	469	10	AI463005	AI463005 yb89g05.x
7	260.8	55.4	423	23	AM587748	AM587748 l0298E02-
8	239.8	50.9	443	19	AV597984	AV597984 AY597984
9	208	44.2	357	19	AM049334	AM049334 UI-M-BH1-
10	207.4	44.0	369	9	AI176343	AI176343 EST121926
11	197.4	41.9	342	13	AI835755	AI835755 UI-M-A10-
12	191.6	40.7	335	2	AV066410	AV066410 AV066410
13	173.4	36.8	289	2	AA245600	AA245600 m330a01.t
14	166.8	33.4	505	8	AI104615	AI104615 u669c02.y
15	155.6	33.0	574	19	AV097985	AV097985 AY597985
16	153.8	32.7	294	15	AV072353	AV072353 AV072353
17	153.8	32.7	354	12	AI642457	AI642457 v80BD10.x
18	153.4	32.6	292	15	AV0653007	AV0653007 AV063007
19	151.6	32.2	287	15	AV0650008	AV0650008 AV065008
20	148.4	31.5	276	15	AV078115	AV078115 AV078115
21	144	31.4	285	15	AV032583	AV032583 AV032583
22	144	30.6	306	15	AV066911	AV066911 AV069683
23	142.4	30.2	300	16	AV186683	AV186683 AV169683
24	139.4	29.6	300	17	AV239413	AV239413 AV239413
25	138.4	29.4	294	15	AV067717	AV067717 AV067717
26	138	29.3	299	15	AV067682	AV067682 AV067682
27	135.6	28.8	293	15	AV076434	AV076434 AV076434
28	130.4	27.7	279	15	AV087765	AV087765 AV087765
29	124.8	26.5	281	21	AM338525	AM338525 xw80B3.x
30	124.8	26.5	267	21	AM338525	AM338525 xw80B3.x
31	117.2	24.9	259	15	AV077144	AV077144 AV071444
32	114	24.2	549	20	AM151778	AM151778 xf69b11.x
33	92	19.5	515	13	AI800476	AI800476 t141h05.x
34	78	16.6	655	96	AO377284	AO377284 RPtC11.16
35	63.8	13.5	325	20	AM142292	AM142292 EST292531
36	57.2	12.1	188	15	AV077488	AV077488 AV077488
37	56.6	12.0	488	6	AI129421	AI129421 qc38g11.x
38	54.2	11.5	186	18	AV328761	AV328761 AV328761
39	49.6	10.5	309	38	N83242	N83242 K4692P Huma
40	47.6	10.1	438	9	AI247015	AI247015 qx52c10.x
41	42.8	9.1	188	15	AV069285	AV069285 AV069285
42	39.6	8.4	413	99	AO592903	AO592903 HS_543_A
43	37.6	8.0	442	1	AA129331	AA129331 zn85B03.s
44	37.6	8.0	1101	112	CMS00396	AI0633921 Dirosophi1
45	37.4	7.9	751	23	AM687654	AM687654 NF011G05R

ALIGNMENTS

LOCUS	AA930362	603 bp	MRNA	EST	23-APR-1998
DEFINITION	v559t07.r1 Strataene mouse skin (#937313) Mus musculus cDNA clone				
IMAGE:	1150597 5' similar to gb:D49949 Mouse mRNA for IGIF precursor				
POLYPEPTIDE	(MOUSE) ; mRNA sequence.				
ACCESSION	AA930362				
VERSION	AA930362.1				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria				
AUTHORS	1 (bases 1 to 603)				
	Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.				
TITLE	The Washu-HHMI Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/Mouse EST Project Washu-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:652805 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 445. Location/Qualifiers 1..603 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:1150597" /clone_lib="Strataene mouse skin (#937313)" /tissue_type="whole skin" /sex="females" /dev_stage="11 weeks old" /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcORI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTATTTTTTTTTTTT 3'"				
BASE COUNT	197 a	111 c	132 g	163 t	
ORIGIN					
Query Match	98.9%	Score 465.8	DB 7	Length 603	
Best Local Similarity	99.2%	Pred. No. 1e-115	3	Indels 0	Gaps 0
Matches 467	Conservative 1	Mismatches 3			
QY	1	AACCTTGCCGACCTCAGTTCATACACCGCAGTATACGGAATTAATGACCAAGTTC	60		
Db	5	AACCTTGCCGACCTCAGTTCATACACCGCAGTATACGGAATTAATGACCAAGTTC	64		
QY	61	TTGCTGACAAAGACAGCGCTGTTCGAGGATGACGATATTTGATCAAACTGCAG	120		
Db	125	GAACCCAGACAGCAGTATATATATATATATATATATATATATATATATATATAT	184		
QY	121	GAACCCAGACAGCAGTATATATATATATATATATATATATATATATATATATAT	180		
Db	185	GTGACCCCTCTCTGTGAAGATAGTAAATATGCTACCTCTCTGTGAAGACAGATAT	244		
QY	181	GTGACCCCTCTCTGTGAAGATAGTAAATATGCTACCTCTCTGTGAAGACAGATAT	240		
Db	241	TGCTTTGAGGAATGATCCACCTGGAATATATGATATATATATATATATATATAT	300		

RESULT 5
AA237736 434 bp mRNA EST 03-MAR-1997
LOCUS mx23901.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:681648 5'
DEFINITION similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide
(MOUSE);, mRNA sequence.
ACCESSION AA237736
VERSION AA237736.1 GI:1861775
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 434)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:421352
putative full length read
vector to vector length is 437
Seq primer: -28m13 rev2 ET from Amerham.
Location/Qualifiers
1. 434
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681648"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGAATCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 139 a 79 c 92 g 124 t
ORIGIN

Query Match 65.5%; Score 308.6; DB 2; Length 434;
Best Local Similarity 99.7%; Pred. No. 3e-73;
Matches 308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 163 GAAGTAGAGAGAGCTGGTGGACCCCTCTGTGAGAGATGATAAAGTCTACCCCTCC 222
|||||
DB 1 GAAGTAGAGAGAGCTGGTGGACCCCTCTGTGAGAGATGATAAAGTCTACCCCTCC 60
|||||

QY 223 TGTAGAGACAGATCATTTCTTTGAGGAATGATGATCCACCTGAAATATGATGATATA 282
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DB 61 TGTAGAGACAGATCATTTCTTTGAGGAATGATGATCCACCTGAAATATGATGATATA 120
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QY 283 CAAAGTATCTCATATTTCTTTGAGGAATGATGATCCACCTGAAATATGATGATATA 342
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DB 121 CAAAGTATCTCATATTTCTTTGAGGAATGATGATCCACCTGAAATATGATGATATA 180
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QY 343 TCTTCACTGTATGAGAGACACTTCTGCTTCCCAAAAGAGATGATGCTTCAACTC 402
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DB 181 TCTTCACTGTATGAGAGACACTTCTGCTTCCCAAAAGAGATGATGCTTCAACTC 240
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QY 403 ATTTCGAAAAAAGAGATGATAAATGGGATTAATCTGATATGTTCACTCTCACTA 462
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DB 241 ATTTCGAAAAAAGAGATGATAAATGGGATTAATCTGATATGTTCACTCTCACTA 300
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QY 463 CATCAAGT 471
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DB 301 CATCAAGT 309
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RESULT 6
AI463005 469 bp mRNA EST 09-MAR-1999
LOCUS VB89g05.x1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:764216
DEFINITION 3' similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide
(MOUSE);, mRNA sequence.
ACCESSION AI463005
VERSION AI463005.1 GI:4317035
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 469)
Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurr, R., Ritter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Maria M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:465136
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 324.
Location/Qualifiers
1. 469
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:764216"
/clone_lib="Soares mouse 3NDMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

BASE COUNT 132 a 99 c 90 g 144 t
ORIGIN

Query Match 58.2%; Score 274; DB 10; Length 469;
Best Local Similarity 90.7%; Pred. No. 6.9e-64;

ethanol-precipitation. The cDNAs were ligated to lene-linker L1-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Plao."

DB	BASE COUNT	ORIGIN
OY	116 a	84 c
OY		81 g
OY		142 t

Query Match	Score	DB	Length
Best Local Similarity	94.9%	Pred. No. 2.5e-60	
Matches 279; Conservative	1;	Mismatches 13;	Indels 1; Gaps 1

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DB <td>423</td> <td>CTGTGACCCCTCTGTGGAAGATAGTAAATGCTACCTCTCTCTGTGAAGACCAAGATCA<td>364</td></td>	423	CTGTGACCCCTCTGTGGAAGATAGTAAATGCTACCTCTCTCTGTGAAGACCAAGATCA <td>364</td>	364
OY <td>239</td> <td>TTTCTTTGAGGAATGATCCACCTGGAATATTCATGATATACAAAGTGATTCATAT</td> <td>304</td>	239	TTTCTTTGAGGAATGATCCACCTGGAATATTCATGATATACAAAGTGATTCATAT	304
OY <td>363</td> <td>TTTCTCTGAGGAATGATCCACCTCAAAATTTGATGATATACAAAGTGATTCATAT</td> <td>358</td>	363	TTTCTCTGAGGAATGATCCACCTCAAAATTTGATGATATACAAAGTGATTCATAT	358

QY	295	TCGATCAGAAACGTTTCCAGACACACAAGATGGAGTGTGATTTTCACGTGTGAAG	244
Db	303	TCGATCAGAAACGTTTCCAGACACACAAGATGGAGTGTGATTTTCACGTGTGAAG	417
QY	359	GACACTTTTCTCTGCGCCAAAAGAGATGATTCGTTCAAACATCATTCGCG-AAAAAAG	184
Db	243	GACACTTATTTACTCTGCGCCAAAAGAGATGATTCGTTCAAACATCATTCGAAAAAAG	184
QY	418	GATGAAATAGGGGATTAATCTGTATATGTCCTACCTCAATACCTACATCAAACT	471
Db	183	GATGAAATAGGGGATTAATCTGTATATGTCCTACCTCAATACCTACATCAAACT	130

RESULT 8
 AV597984/c 443 bp mRNA EST 06-AUG-2000
 LOCUS AV597984 Bos taurus cartilage fetus Bos taurus cDNA clone
 DEFINITION E1CA035C10.3', mRNA sequence.
 ACCESSION AV597984
 VERSION AV597984.1 GI:9715479
 KEYWORDS EST.

KEYWORDS . EST.
SOURCE .
ORGANISM .
Bos taurus
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Eukaryota; Eumetazoa; Cetiartiodactyla; Ruminantia; Pecora; Bovidae
Mammalia; Bovinae; Bos.
Pages 1 to 443
1
REFERENCE
Sugimori, Y., Hirotsune, S., Takasuga, A., Itoh, R., Itohizono, A. and
Suzuki, H.

TITLE bovine CDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shiitakea Institute of Animal Genetics
Shiitakea, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Okamura, Nishigo
Tel: 81-248-255641
Fax: 81-248-255725
Email: kazu@ccocn.ocn.ne.jp
Single pass sequencing from a polyA-deleted cDNA library.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES location/Qualifiers
SOURCE 1..443

source
/organism="Bos taurus"
/db_xref="taxon:9913"

Query Match	50.9%;	Score 239.8;	DB 19;	Length 443;
Best Local Similarity	75.5%;	Pred. No. 1.2e-54;		
Matches 324;	Conservative 1;	Mismatches 98;	Indels 6;	Gaps 2

oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA library Preparation: M.B. Soares lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence 18-84, >MSTP#1/R/MaIR
Seq primer: M13 Forward
POLYA-Tes.

Location/Qualifiers
1. .357

```

source
1. 357
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_uid="M-BH1-amr-f-09-0-01"
/clone_id="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pUT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a substracted library derived
from the NIH_BMAP_M_S1, which in turn is a substracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB_NIH_BMAP_M_S2
TAG_TISSUE-brain-stems
TAG_SEQ-TCATG"
100 a 71 c 59 g 127 t
BASE COUNT
ORIGIN

```

```

Best Local Similarity: 100.0%; Pred. NO. 4,5e-46;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Accession	Sequence	Position
Db	357 TGAAGATTTTATGATGATATACAAAGATGCTCATATTCTTTCGAAACCGTGTTCCAGGACA	298
Qy	324 CAACAAGATGAGTTGAAATCTTCACCTGTATGCAAGACACTTCTGCTGGCAAAAGGA	383
Db	297 CAACAAGTTGAGTTGAAATCTTCACCTGTATGCAAGACACTTCTGCTGGCAAAAGGA	238
Qy	384 AGATGATCTCTTCAACATCATCTTGTAAAAAAGCATGAAATGGCGATTAATCTGTAAAT	443
Db	237 AGATGATCTCTTCAACATCATCTTGTAAAAAAGCATGAAATGGCGATTAATCTGTAAAT	178

[illegible]

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
A1176343	A1176343.1	EST.	Rattus sp.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Wed Nov 22 11:24:55 2000

us-09-050-249-1.rst

Page 8

COMMENT
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd, Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 1706
Email: mestrang.nih.gov

Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 369)
Lee, N.H., Gloder, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
Gene Index
Unpublished (1998)
On Oct 8, 1998 this sequence version replaced g1:3726981.
Other ESTs: TC49330
Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) 838-3529
Fax: (301) 838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..369
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone_lib="Normalized rat ovary, Bonto Soares"
/note="Organ: ovary; Vector: pT73pac; Site_1: EcoRI;
Site_2: NotI"

FEATURES
SOURCE
BASE COUNT 114 a 64 c 61 g 130 t
ORIGIN
Query Match 44.0%; Score 207.4; DB 9; Length 369;
Best Local Similarity 91.3%; Pred. No. 6.6e-46; Indels 0; Gaps 0;
Matches 220; Conservative 0; Mismatches 21;

Y 231 CAAGATGATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 290
DB 369 CAATATGATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 310
Y 291 TGTATATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 250
DB 309 TTTCATATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 410
Y 351 GTATGAGACACTTCTGCTGCTCCAAAGAGATGATGCTTCAAACTGATCTGA 410
DB 249 GTATGAGACACTTCTGCTGCTCCAAAGAGATGATGCTTCAAACTGATCTGA 190
Y 411 AAAAAAGATGAAATGGGATTAATCTGTATGCTTCACTCTCACTTCACTCACTCA 470
DB 189 AAGGAAGATGAAATGGGATTAATCTGTATGCTTCACTCTCACTTCACTCACTCA 130
Y 471 T 471
DB 129 T 129

RESULT 11
AI835755 342 bp mRNA EST 14-JUL-1999
LOCUS AI835755 342 bp mRNA EST 14-JUL-1999
DEFINITION U1-M-A10-aan-g-11-0-UI 3', mRNA sequence.
ACCESSION AI835755.1 GI:5469968
VERSION AI835755.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
TITLE Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477

FEATURES
SOURCE
BASE COUNT 98 a 68 c 55 g 121 t

Location/Qualifiers
1..342
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="U1-M-A10-aan-g-11-0-UI"
/clone_lib="NIH-BMAP_MBS"
/dev_stage="27-32 days"
/lab_host="D10B (Life Technologies)"
/note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH-BMAP_MBS library is a non-normalized library
constructed from mouse brain stems. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories.
TAG: LIB-NIH-BMAP_MBS
TAG: TISSUE-brain-stems
TAG-SEQ-TACAG"

Query Match 41.9%; Score 197.4; DB 13; Length 342;
Best Local Similarity 99.5%; Pred. No. 3.2e-43; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 1;

Y 273 TGATGATTAAGAGTGTCTATATCTTTCAGAAAGCTGTCAGGACCAACAGAT 332
DB 342 TGATGATTAAGAGTGTCTATATCTTTCAGAAAGCTGTCAGGACCAACAGAT 283
Y 333 GGAGTTGATCTTCAGTGTATGAAGACACTTCTGCTGCTCCAAAGAGATGATGC 392
DB 282 GGAGTTGATCTTCAGTGTATGAAGACACTTCTGCTGCTCCAAAGAGATGATGC 223
Y 393 TTTCATATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 452
DB 222 TTTCATATTCCTTGGAGAAATGATCCAGAAATATGATGATATCAAACTGA 163
Y 453 CACTAATCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 471
DB 163 CACTAATCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 144

RESULT 12
AV066410 335 bp mRNA EST 24-JUN-1999
LOCUS AV066410 335 bp mRNA EST 24-JUN-1999
DEFINITION AV066410 Mus musculus small intestine C57BL/6J adult Mus musculus
CDNA clone 2010109E01, mRNA sequence.
ACCESSION AV066410

VERSION AV066410.1 GI:5186238
 EST
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, Y., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsumu, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@frc.riken.go.jp
 Thermolabile and thermolabile activation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3435-3460 (1998))
 Please visit our web site (<http://genome.etc.riken.go.jp>) for further details.

FEATURES
 source location/Qualifiers
 1..335
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="2010109E01"
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 /sex="male"
 /tissue-type="small intestine"
 /dev-stage="adult"
 /dev-stage="67 g 100 t"

BASE COUNT 109 a 59 c 67 g 100 t
 ORIGIN

Query Match 40.7%; Score 191.6; DB 15; Length 335;
 Best Local Similarity 95.6%; Pred. No. 1.2e-41;
 Matches 197; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 266 AAAATATGATGATATACAAAGTATCATATCTTTCAGAAAGCTGTCAGACACA 325
 1 AAAATATGATGATATACAAAGTATCATATCTTTCAGAAAGCTGTCAGACACA 60
 DB 1
 OY 336 ACAAGATGAGTGTGATCTTCACTGATGAAGACACTTCTTCTGCCAAAGAG 385
 61 ACAAGATGAGTGTGATCTTCACTGATGAAGACACTTCTTCTGCCAAAGAG 120
 DB 61
 OY 386 ATGATGCTTCAACTCATCTTGAAGAAAGGATGAAGGATGAAGTGAATGT 445
 121 ATGATGCTTCAACTCATCTTGAAGAAAGGATGAAGGATGAAGTGAATGT 180
 DB 121
 OY 446 TCACCTCCTCACTTACATCAAGT 471
 181 TCACCTCCTCACTTACATCAAGT 206
 DB 181

RESULT 13
 AA245600 289 bp mRNA EST 10-MAR-1997
 LOCUS AA245600
 DEFINITION mx30a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:661672 5'
 similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide (MOUSE);, mRNA sequence.
 ACCESSION AA245600

VERSION AA245600.1 GI:1876519
 EST
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Geisler, S., Kucaba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Mair, M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, R., Stepien, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wille, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:421376
 Trace considered overall poor quality
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.

FEATURES
 source location/Qualifiers
 1..289
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:661672"
 /clone.lib="Soares mouse NML"
 /tissue-type="liver"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dCT) primer [5' TGTACCACTCATGAGGAGGCGGCGGCAATCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 51 c 75 g 86 t
 ORIGIN

Query Match 36.8%; Score 173.4; DB 2; Length 289;
 Best Local Similarity 79.2%; Pred. No. 9.5e-37;
 Matches 229; Conservative 1; Mismatches 57; Indels 2; Gaps 2;

OY 167 TAAGGACATGCTGTGACCTCTCTGTGAGAGATAGTAATATCTACCTCTCCGTA 226
 1 TAGTAGGACATGCTGTGACCTCTCTGTGAGAGATAGTAATATCTACCTCTCCGTA 60
 DB 1
 OY 227 AGAAGATGATATTCCTTCACTGATGAAGGATGATGATGATGATGATGATGATGAT 285
 61 AGAAGATGATATTCCTTCACTGATGAAGGATGATGATGATGATGATGATGATGAT 120
 DB 61
 OY 286 AGTATCTCATATCTTTCAGAAAGCTGTTCCAGACACAAGATGAGTGTGA-ATC 344
 121 AGTATCTCATATCTTTCAGAAAGCTGTTCCAGACACAAGATGAGTGTGA-ATC 180
 DB 121
 OY 345 TTCACCTGATGAGACACTTCTTCTGCCAAAGAGATGATGCTTCAAGTAT 404
 181 TTCACCTGATGAGACACTTCTTCTGCCAAAGAGATGATGCTTCAAGTAT 240
 DB 181

OY 405 TCTGAAAAAAGATGAAATGGGATGAATCTGTAATGTCCTCTC 453
 241 TCTGAAAAAAGATGAAATGGGATGAATCTGTAATGTCCTCTC 289
 DB 241

Db 456 GAAACCCAGACGAGTGTATATACATGTACAAAGCAAGGAGTAG 503

[illegible]

REFERENCE	TITLE	JOURNAL	COMMENT
Bovidae; Bovinae; Bos. 1 (bases 1 to 574) Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jichonzo, A. and Suzuki, H.	bovine cDNA sequencing Unpublished (2000) Contact: Yoshihazu Sugimoto		Animal Genetics, Dept of Animal Genetics National Institute of Livestock and Fisheries Sciences Tsukuba 305-0856, Japan Tel: 0298-538-961-8061, Japan

Unpublished (2000).
JOURNAL
COMMENT.
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Animal Genetics
Shirakawa Institute of Animal Genetics
Shirakawa, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ccocor.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers

```

FEATURES
  source
    Email: kazus@xq.riken.go.jp
    Single pass sequencing:
    This clone was obtained from a polyA-deleted cDNA library
    Location/Qualifiers
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        /organism="Bos taurus"
        /mol_type="cDNA"
        /db_xref="GeneID:1013"

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1. .505
/organism="Mus musculus"
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173 a 120 c

Query Match	Similarity	Pred. No.	Indels	Gaps
Best Local	92.98%	7,556	75	3
Matches	213	Mismatches	1	Indels
	Conservative			Gaps

[illegible]

143 a 1220

Query Match	Pred. No.	6.8e-35	Indels	Gaps
Best Local Similarity	98.8%		2	
Matches	168	0	Mismatches	

1 AACTTGGCCGACTTCACIGTACACCCCC.....
|||||
|||CTGTATCAACCGCAGTATACGGAATATAAATGACCACAATTCTC 395

Db 336 AACTTGGCCGACCTTACAGTA...
.....AACCAACTGTGTTCAGCATATGA
.....

61 TTCTGTGACAAAGAGCAGCCAGT 45

Db 396 TTGTTGACAAAGAGC... 170

 $\cdot QY \cdot$

Search completed: November 21, 2000, 21:13:23
Job time: 15485 sec